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OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 16:01:57 ; Search time 97146 Seconds
(without alignments)
17846.554 Million cell updates/sec

Title: US-09-728-552A-3_COPY_1_40000
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION Sequence 3 from Patent WO9851790.
ACCESSION AX033911
VERSION AX033911.1 GI:10280479
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Cancilla,M.R., Choo,K.H. and Du,S.D.
TITLE A novel nucleic acid molecule
JOURNAL Patent: WO 9851790-A 3 19-NOV-1998;
CANCILLA MICHAEL ROBERT (AU) ; CHOO KONG HONG ANDY (AU) ; SART

DESIREE DU (AU) ; AMRAD OPERATIONS PTY LTD (AU)

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Best Local Similarity 100.0%; Pred. No. 0;
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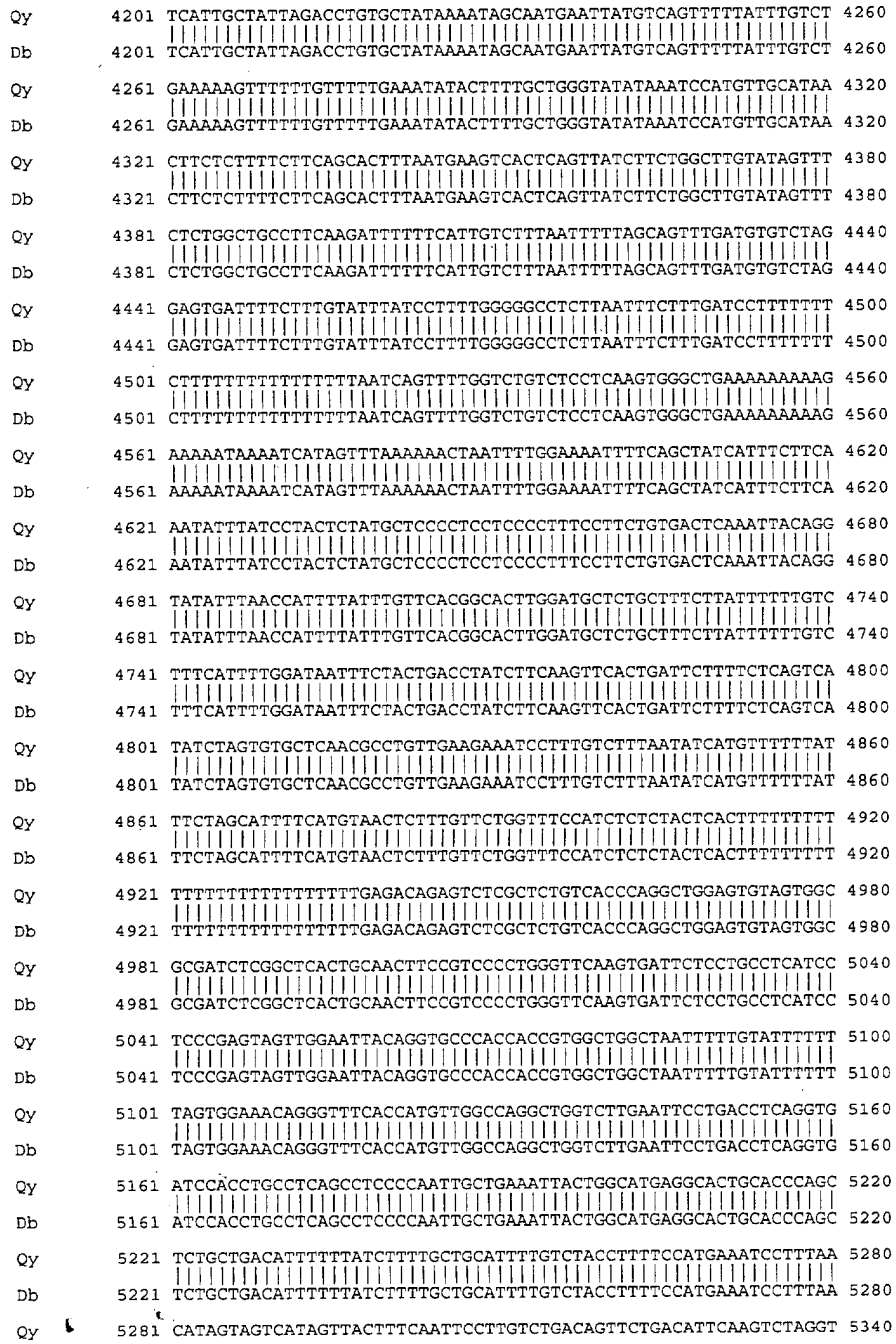
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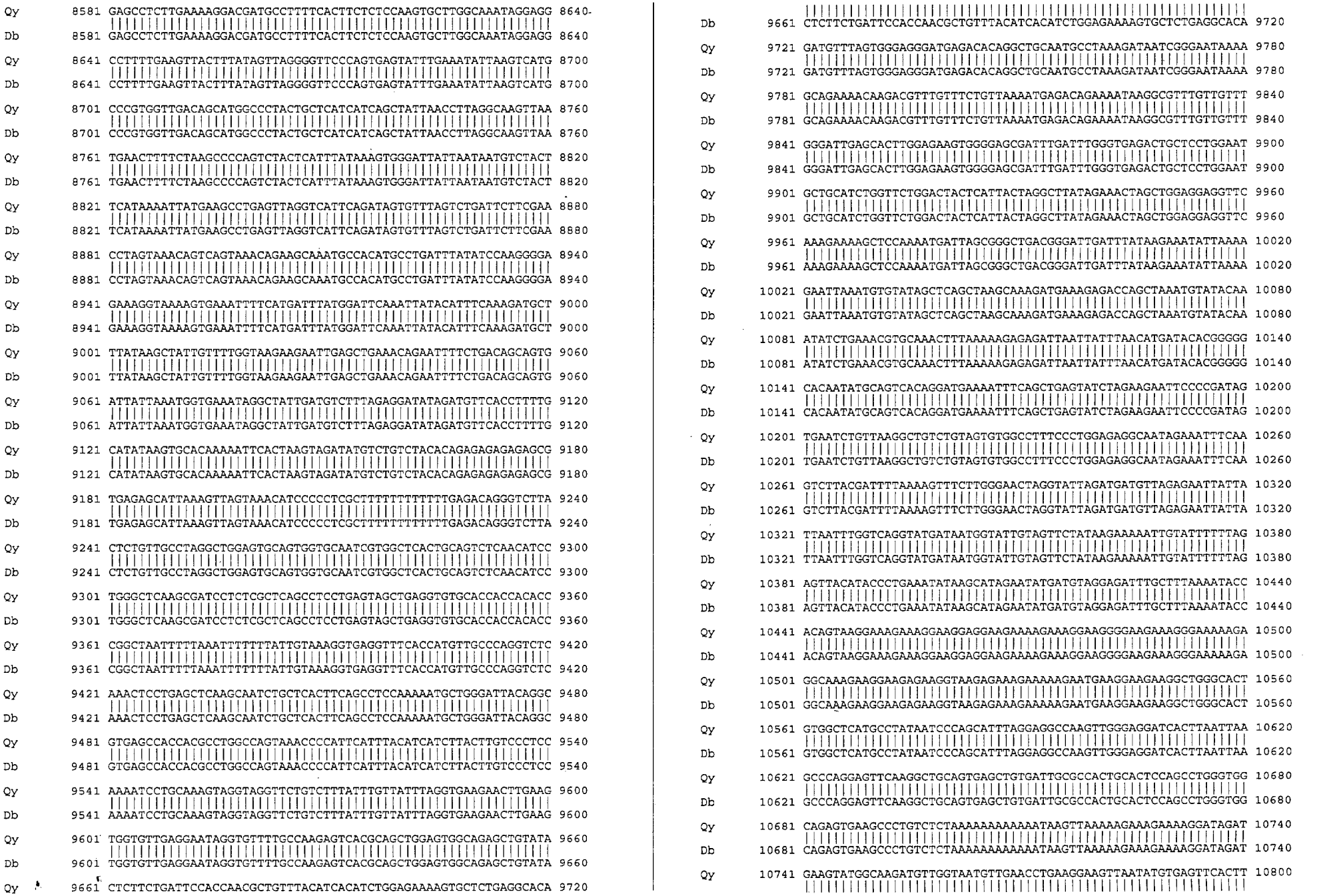
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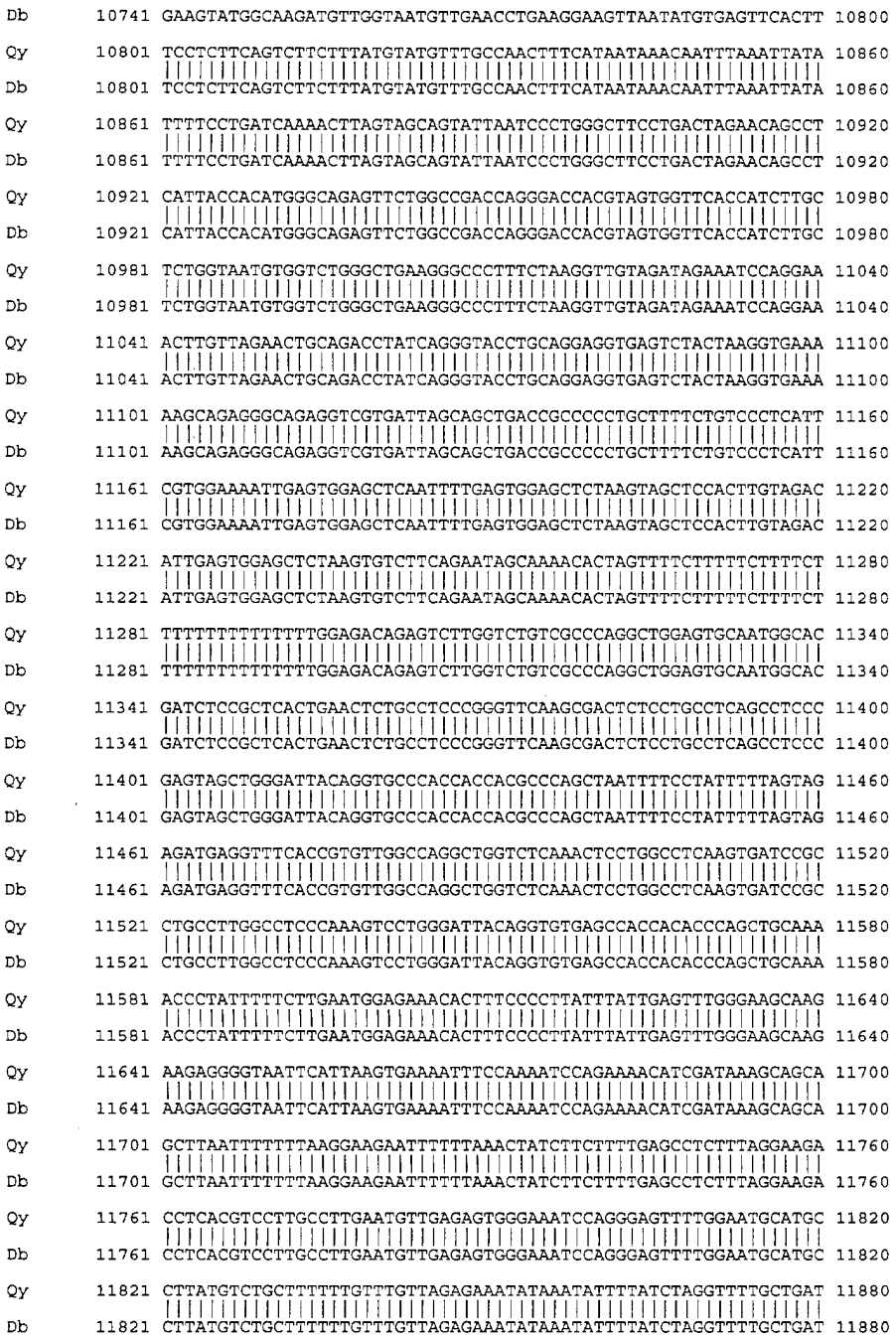
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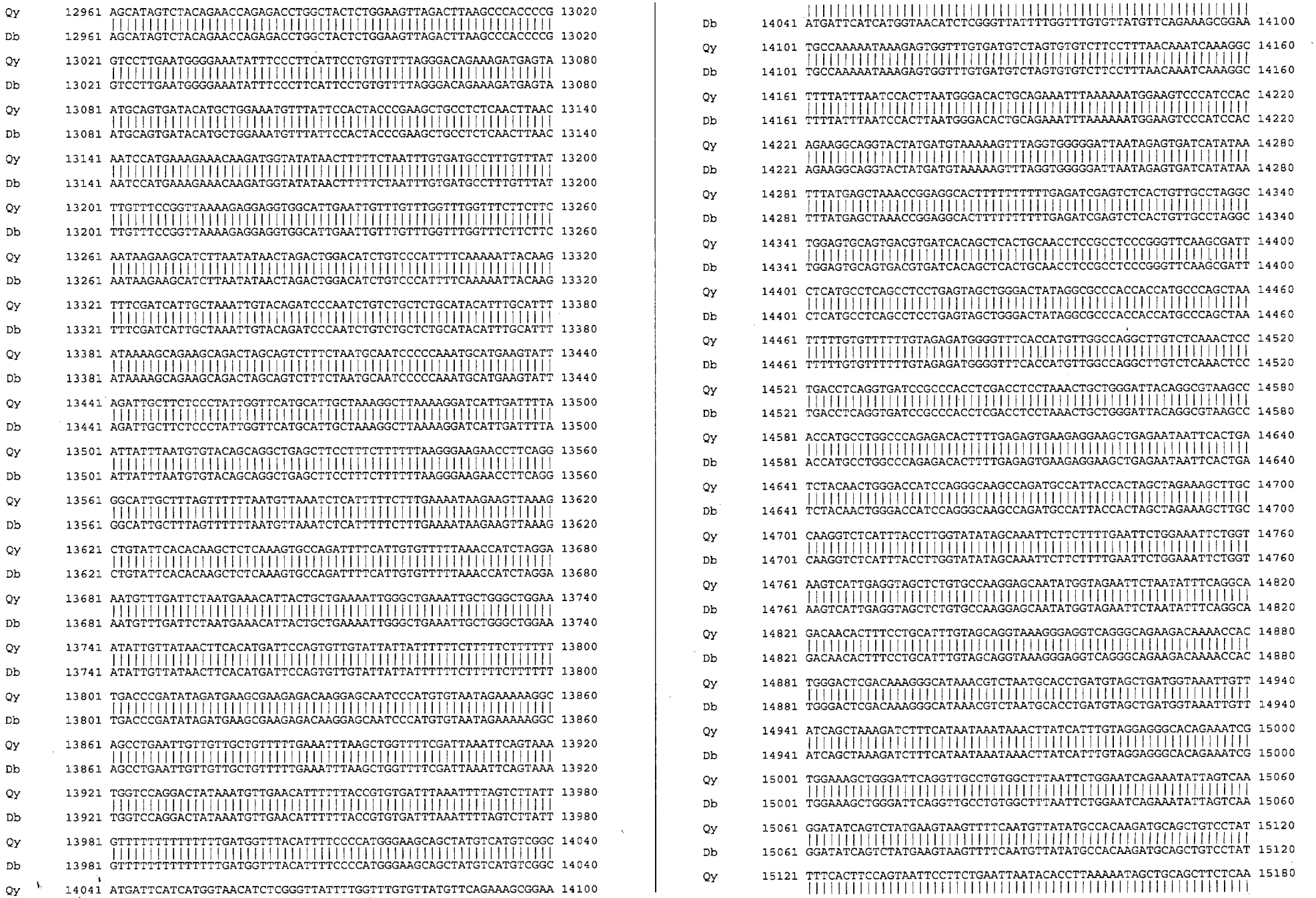

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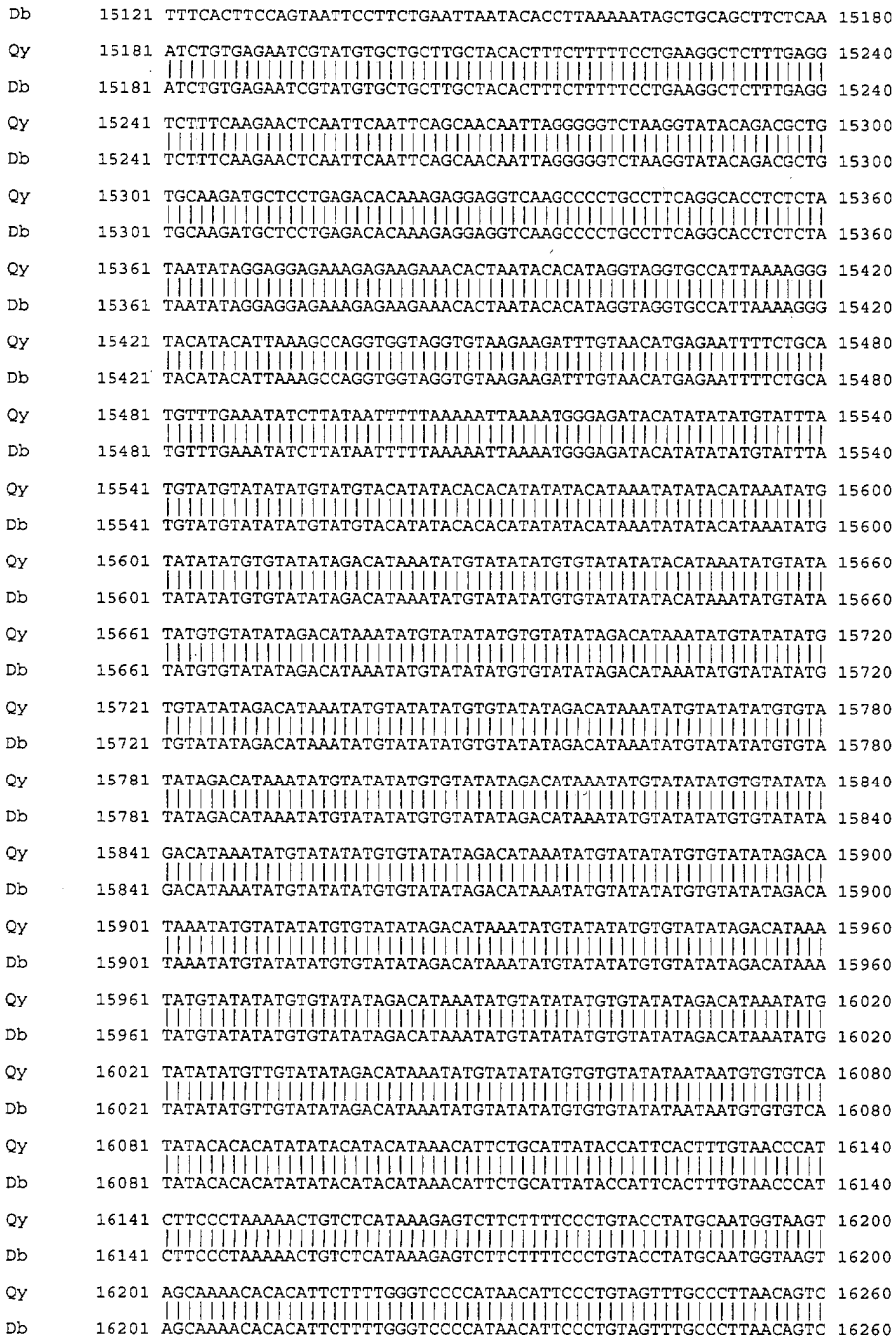
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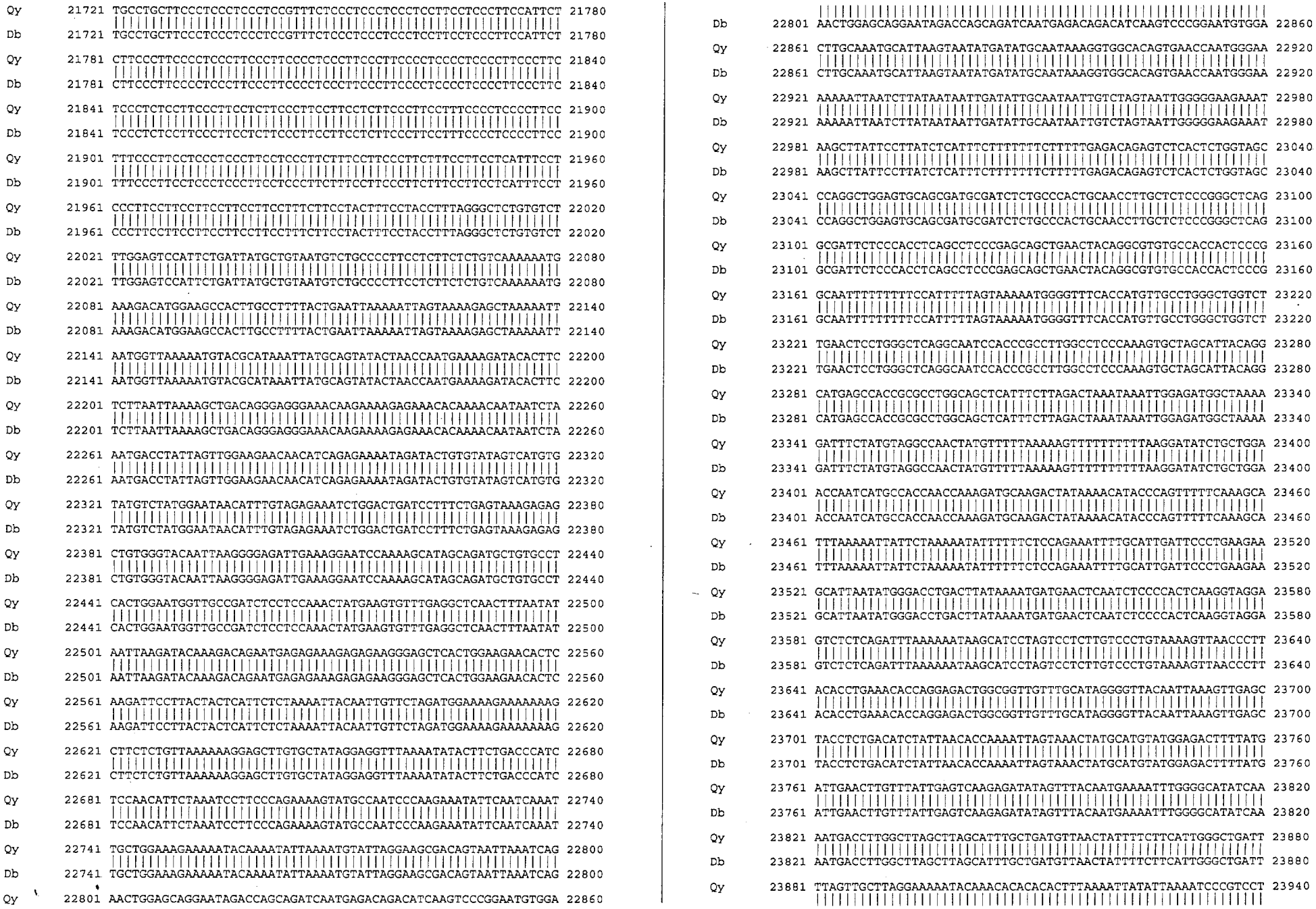
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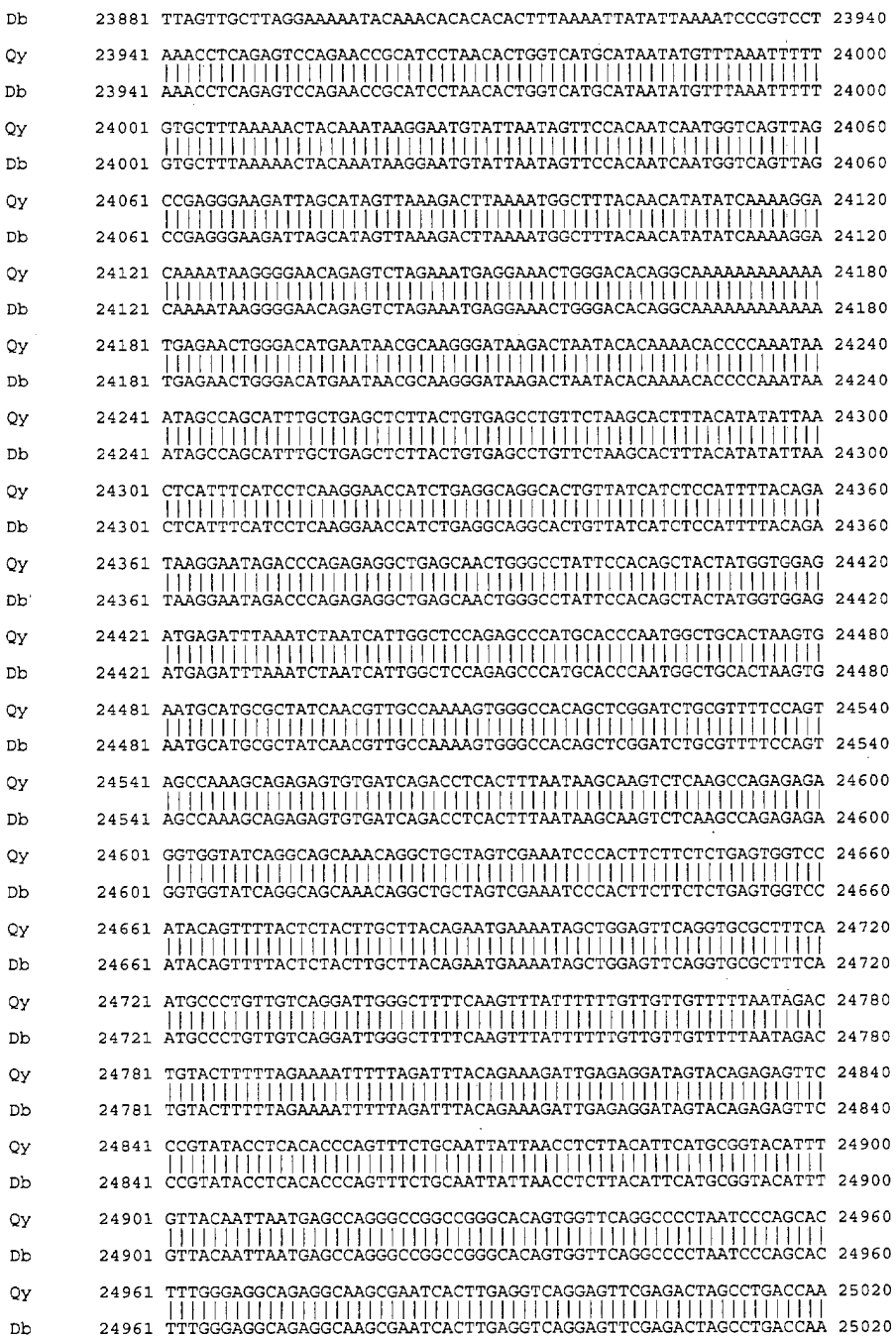
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Qy      19501 TCTTTAAATACTGCTTTTCTCAGCTCAATTGGCTTTCTTCCCTCTGGCAGTCACGTTTCT 19560
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Qy 24721 ATGCCCTGTTGTCAGGATTGGGCTTTTCAAGTTTATTTTTTGTTGTTGTTTTTAATAGAC 24780
Db 24721 ATGCCCTGTTGTCAGGATTGGGCTTTTCAAGTTTATTTTTTGTTGTTGTTTTTAATAGAC 24780
Qy 24781 TGTACTTTTTAGAAAATTTTTAGATTTACAGAAAGATTGAGAGGATAGTACAGAGAGTTC 24840
Db 24781 TGTACTTTTTAGAAAATTTTTAGATTTACAGAAAGATTGAGAGGATAGTACAGAGAGTTC 24840
Qy 24841 CCGTATACCTCACACCCAGTTTCTGCAATTATTAACCTCTTACATTCATGCGGTACATTT 24900
Db 24841 CCGTATACCTCACACCCAGTTTCTGCAATTATTAACCTCTTACATTCATGCGGTACATTT 24900
Qy 24901 GTTACAATTAATGAGCCAGGGCCGGCCGGGCACAGTGGTTCAGGCCCCTAATCCCAGCAC 24960
Db 24901 GTTACAATTAATGAGCCAGGGCCGGCCGGGCACAGTGGTTCAGGCCCCTAATCCCAGCAC 24960
Qy 24961 TTTGGGAGGCAGAGGCAAGCGAATCACTTGAGGTCAGGAGTTCGAGACTAGCCTGACCAA 25020
Db 24961 TTTGGGAGGCAGAGGCAAGCGAATCACTTGAGGTCAGGAGTTCGAGACTAGCCTGACCAA 25020
Qy 25021 CATGGTAAACCCTTTCTGTACTAAAAATACAAAAAATTAGCCAGGCATGGTGCTGGTTGC 25080
Db 25021 CATGGTAAACCCTTTCTGTACTAAAAATACAAAAAATTAGCCAGGCATGGTGCTGGTTGC 25080
Qy 25081 CTGTATTCCCAGATACTCAGGAGGCTGAGGCACAAGAATTGCTTGAACCAGGGAGGCGGA 25140
Db 25081 CTGTATTCCCAGATACTCAGGAGGCTGAGGCACAAGAATTGCTTGAACCAGGGAGGCGGA 25140
Qy 25141 GGTTGCAGTAAGCCGAGATCGTGCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCC 25200
Db 25141 GGTTGCAGTAAGCCGAGATCGTGCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCC 25200
Qy 25201 ATCAAAAAAAAAAAAAAAAAAAAAAAGAAGGAAGGAAGGAAGGAAAATTAATGAGCCAATA 25260
Db 25201 ATCAAAAAAAAAAAAAAAAAAAAAAAGAAGGAAGGAAGGAAGGAAAATTAATGAGCCAATA 25260
Qy 25261 TTGAGACATTATTATTACTAAAGTCCATGCTTTATGCAGATTTTCTTAGTTTTTACCTGC 25320
Db 25261 TTGAGACATTATTATTACTAAAGTCCATGCTTTATGCAGATTTTCTTAGTTTTTACCTGC 25320
Qy 25321 TGTCATTTTTCAGTTCCAGGAATGCATTCAGGATGCCATACCACATTTAGTTCTCATATC 25380
Db 25321 TGTCATTTTTCAGTTCCAGGAATGCATTCAGGATGCCATACCACATTTAGTTCTCATATC 25380
Qy 25381 TGCTTAGGCTCCTCTTGGCTAGACTGAGTTTTAATCTACTTTCTGCAGAGCCTGAGAACT 25440
Db 25381 TGCTTAGGCTCCTCTTGGCTAGACTGAGTTTTAATCTACTTTCTGCAGAGCCTGAGAACT 25440
Qy 25441 TTAGCATAATTTCCTTGGAAATTACAGCTCAATATTTTCAAGCACTTATACAAACAGCCT 25500
Db 25441 TTAGCATAATTTCCTTGGAAATTACAGCTCAATATTTTCAAGCACTTATACAAACAGCCT 25500
Qy 25501 AATGTTACGTTGGCCCATAACAGTGTTTCAAGGTAATAAACTTCTTTGTTTTCTGTGCCG 25560
Db 25501 AATGTTACGTTGGCCCATAACAGTGTTTCAAGGTAATAAACTTCTTTGTTTTCTGTGCCG 25560
Qy 25561 ATTGAAAGAACTGCTGCTTAGCCTCCTGCCAGATGATGAACTGGGTACACACGAGCATTT 25620
Db 25561 ATTGAAAGAACTGCTGCTTAGCCTCCTGCCAGATGATGAACTGGGTACACACGAGCATTT 25620
Qy 25621 TTCCAGGTAAAGCATATTTCGTGCGACTTCTTAAGCTGCAGCCTTATATGCAATAATTGT 25680
Db 25621 TTCCAGGTAAAGCATATTTCGTGCGACTTCTTAAGCTGCAGCCTTATATGCAATAATTGT 25680
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Db 25681 CCATTTACAAGACTTATGTTCGAATTTCAGGCACTCTGTTTTCACTAACCATATCCTTCA 25740
Qy 25741 ACTTTGATAAGTACTGCTTTAATCAACTCAGAAAATTTAACTTGACTAATTTTTTTTCAC 25800
Db 25741 ACTTTGATAAGTACTGCTTTAATCAACTCAGAAAATTTAACTTGACTAATTTTTTTTCAC 25800
Qy 25801 CATCAGTTTTTTTTCTGTTGACTCTTTCTCCTTTTTCTGTTTGCCCAGAAACATGCTCAG 25860
Db 25801 CATCAGTTTTTTTTCTGTTGACTCTTTCTCCTTTTTCTGTTTGCCCAGAAACATGCTCAG 25860
Qy 25861 GATTCTCTCAGGCTTTAAAAAATGAAAAAATGTTTCCTGCAATCTAGTTACTCCTTGATT 25920
Db 25861 GATTCTCTCAGGCTTTAAAAAATGAAAAAATGTTTCCTGCAATCTAGTTACTCCTTGATT 25920
Qy 25921 CTCTTGTTCTGTTTATCGCTGGAATTCTTGAAAGCTTGGTGTATTAGTCTTTTTTCATGC 25980
Db 25921 CTCTTGTTCTGTTTATCGCTGGAATTCTTGAAAGCTTGGTGTATTAGTCTTTTTTCATGC 25980
Qy 25981 TGCTGATAAAGATATACCTGAGACTGGATAATTTATAAAGAAAAAGAGGTTTAATGGACT 26040
Db 25981 TGCTGATAAAGATATACCTGAGACTGGATAATTTATAAAGAAAAAGAGGTTTAATGGACT 26040
Qy 26041 CACAGTTCCACGTGGCTGAGGAAGCCTCACAATCATGGTGGAAGGCAAAAGGCATGTCTT 26100
Db 26041 CACAGTTCCACGTGGCTGAGGAAGCCTCACAATCATGGTGGAAGGCAAAAGGCATGTCTT 26100

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Qy      26101 ACATGGCAGCAGACAAGAGAGAATGAGAACCAAGGGATTTCCCCTTATAAAACCATCAGA 26160
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Db      26101 ACATGGCAGCAGACAAGAGAGAATGAGAACCAAGGGATTTCCCCTTATAAAACCATCAGA 26160

Qy      26161 TCTTGTGAGACTTATTCACTACCACAAGAACAATATGGGGTAAACCGCCCCCATGATTCA 26220
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Db      26161 TCTTGTGAGACTTATTCACTACCACAAGAACAATATGGGGTAAACCGCCCCCATGATTCA 26220

Qy      26221 ATTATCTCCCACCGGGGGCCCTCCCACAACACGTGGGAATTATGGGAGCTACAATTCAAGA 26280
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Db      26221 ATTATCTCCCACCGGGGGCCCTCCCACAACACGTGGGAATTATGGGAGCTACAATTCAAGA 26280

Qy      26281 TGACATTTGGGTGGGGACATGGCCAAACCATATCACCTGGCCTATAGCATTATTTCCATT 26340
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Db      26281 TGACATTTGGGTGGGGACATGGCCAAACCATATCACCTGGCCTATAGCATTATTTCCATT 26340

Qy      26341 TCTTCCCCATCCTTTTATTCCTCAAACCGGTACAACCAGACCTCTTTTTTTTTTTTTCTA 26400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26341 TCTTCCCCATCCTTTTATTCCTCAAACCGGTACAACCAGACCTCTTTTTTTTTTTTTCTA 26400

Qy      26401 CCTGAAACTGCTCTTTTGAGGGTAGCTGATAAGTCCAAAATACTGTCACCTTTTCTCAAT 26460
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Db      26401 CCTGAAACTGCTCTTTTGAGGGTAGCTGATAAGTCCAAAATACTGTCACCTTTTCTCAAT 26460

Qy      26461 TCCGTTCCTTCTTATGCCTTTGGAGCAATTGACTGTGTTGGTTGCCCCCTCCTTTAAAGT 26520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26461 TCCGTTCCTTCTTATGCCTTTGGAGCAATTGACTGTGTTGGTTGCCCCCTCCTTTAAAGT 26520

Qy      26521 GTCTCTCACTTGGTTTTATGACTAATGATGATTTTCTTTTTCCTCTCTAAACATTCCGCT 26580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26521 GTCTCTCACTTGGTTTTATGACTAATGATGATTTTCTTTTTCCTCTCTAAACATTCCGCT 26580

Qy      26581 ATCTTTTTAGCTTCCCTTCCCCCTCCCATCCCCTAAATGTCCTTGTTTCCCAGAATCTGC 26640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26581 ATCTTTTTAGCTTCCCTTCCCCCTCCCATCCCCTAAATGTCCTTGTTTCCCAGAATCTGC 26640

Qy      26641 CTCACCTCTTTGACTTCTCTATGCCCTGTCATTCACTCATGGGTCTTTATTACATTATTG 26700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26641 CTCACCTCTTTGACTTCTCTATGCCCTGTCATTCACTCATGGGTCTTTATTACATTATTG 26700

Qy      26701 CATCTGTGTCAATAACTCTGGTCTTTCTGTTAAGTTCCAGTCTCCCATTTTCAAATGTCC 26760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26701 CATCTGTGTCAATAACTCTGGTCTTTCTGTTAAGTTCCAGTCTCCCATTTTCAAATGTCC 26760

Qy      26761 CCAGACATTTCCAATTGAGTATCTCTCCAATGTATTTAACCTGCTAAATATCTAACACAT 26820
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Db      26761 CCAGACATTTCCAATTGAGTATCTCTCCAATGTATTTAACCTGCTAAATATCTAACACAT 26820

Qy      26821 AATCTTTCCCATCAAATCGTTTCCTCTTAAGCTTTTCGTTATTTCCTATTAGACTCCTGC 26880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26821 AATCTTTCCCATCAAATCGTTTCCTCTTAAGCTTTTCGTTATTTCCTATTAGACTCCTGC 26880

Qy      26881 ACTTCTCCCAGGAGCCCAGACTTAAAACCTTGAATTTCTCACCATAACCTCTCTTTTGTC 26940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26881 ACTTCTCCCAGGAGCCCAGACTTAAAACCTTGAATTTCTCACCATAACCTCTCTTTTGTC 26940

Qy      26941 TCCCATAATCAATTAGTAGCAAGTGTTATCAATGATTACTTGACAATATCTTTTTCTATT 27000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26941 TCCCATAATCAATTAGTAGCAAGTGTTATCAATGATTACTTGACAATATCTTTTTCTATT 27000

Qy      27001 TCCCTCCCTGCTATGATCATTCATCTAGCAAGAAGAGTTGGCCCTTTGTATCTGTGGTTT 27060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27001 TCCCTCCCTGCTATGATCATTCATCTAGCAAGAAGAGTTGGCCCTTTGTATCTGTGGTTT 27060

Qy      27061 CTGCATCCCTGGATTCAACCAACTGTAGATGGAAAATATTTGAAGAAAAAAGCGTCTATA 27120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27061 CTGCATCCCTGGATTCAACCAACTGTAGATGGAAAATATTTGAAGAAAAAAGCGTCTATA 27120

Qy      27121 CTGAGTATGAAAAAATTTTATTTCTTGTCATTATTCCCTAAACAATACAGTATAACAACT 27180
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Db      27121 CTGAGTATGAAAAAATTTTATTTCTTGTCATTATTCCCTAAACAATACAGTATAACAACT 27180

Qy      27181 ACAGCATTTACACTGTAGCGTATAGATCTTATAATCTAGAAATGATTTCAAGTACACCAT 27240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27181 ACAGCATTTACACTGTAGCGTATAGATCTTATAATCTAGAAATGATTTCAAGTACACCAT 27240

Qy      27241 TATATATAAGGGACTTGAGCATCTGTGAAGTTTGGTATTTGTGGGGCATACTGGGACCAA 27300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27241 TATATATAAGGGACTTGAGCATCTGTGAAGTTTGGTATTTGTGGGGCATACTGGGACCAA 27300

Qy      27301 TTCCCCCATGGATACAGAGGGACAACTATATTTACTCAGTGCTTACTAAATACCAGTTGG 27360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27301 TTCCCCCATGGATACAGAGGGACAACTATATTTACTCAGTGCTTACTAAATACCAGTTGG 27360

Qy      27361 CCAATGTGTTTTTCTTTTTCTGTTTTCCTGTCTTTAGTTTGCCCCTTGCCAATTAATTCA 27420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27361 CCAATGTGTTTTTCTTTTTCTGTTTTCCTGTCTTTAGTTTGCCCCTTGCCAATTAATTCA 27420

Qy      27421 ATAGTGCTGCCAATGCCAGGTGTACCTTCAGAATATTCTATTCTAATTTTGTCATCTCCA 27480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27421 ATAGTGCTGCCAATGCCAGGTGTACCTTCAGAATATTCTATTCTAATTTTGTCATCTCCA 27480

Qy      27481 AGCTTAAAAATATTTAATGGGCCAGGCGCAGTGGCTCACACTTGTAATCCCAGCATTTTG 27540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27481 AGCTTAAAAATATTTAATGGGCCAGGCGCAGTGGCTCACACTTGTAATCCCAGCATTTTG 27540

Qy      27541 GGAGGCCAAGGGGGGGGTGTATCACTTGAGGTCAGGAGTTCCAGACCAGCCTGGCCAACAT 27600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27541 GGAGGCCAAGGGGGGGGTGTATCACTTGAGGTCAGGAGTTCCAGACCAGCCTGGCCAACAT 27600

Qy      27601 GGCGAAACCCTGTCTCTACAAAAAAGTATAAAAGTTAACCAGGTGCTGGAGCATTTGCCT 27660
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Db      27601 GGCGAAACCCTGTCTCTACAAAAAAGTATAAAAGTTAACCAGGTGCTGGAGCATTTGCCT 27660

Qy      27661 GTGGTCCCAGCTACTCAGGAGGCTGAGGCAGGAAAATCACTTTAATCTGGGAGGTGGAGT 27720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27661 GTGGTCCCAGCTACTCAGGAGGCTGAGGCAGGAAAATCACTTTAATCTGGGAGGTGGAGT 27720

Qy      27721 TTGCAGTGAGCCAAGATCTCTCCACTGCACTCCAGCCTGGGTGACACAGCAAGACTCTAT 27780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27721 TTGCAGTGAGCCAAGATCTCTCCACTGCACTCCAGCCTGGGTGACACAGCAAGACTCTAT 27780

Qy      27781 CTCAAAACAACAATAACAACAACAACGAAAAACATTTAATGGCTGCACCTTGCCTGTGAA 27840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27781 CTCAAAACAACAATAACAACAACAACGAAAAACATTTAATGGCTGCACCTTGCCTGTGAA 27840

Qy      27841 AAATGCATTTCTTGGCCAGATGTGGTGGCTCAAACCTGTAATCCCAACACTTTGGGAAGC 27900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27841 AAATGCATTTCTTGGCCAGATGTGGTGGCTCAAACCTGTAATCCCAACACTTTGGGAAGC 27900

Qy      27901 TAAGGCCAGGAGTTCGAGACGAGCTGGGATATATAGGAAGACACAATCTCTACAAAAAAA 27960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27901 TAAGGCCAGGAGTTCGAGACGAGCTGGGATATATAGGAAGACACAATCTCTACAAAAAAA 27960

Qy      27961 AATCCACAAAATTAGTCAGGCTTATTGTTCATGCCTGTAGTCCCAGGTACTCAGGAGGCT 28020
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Db      27961 AATCCACAAAATTAGTCAGGCTTATTGTTCATGCCTGTAGTCCCAGGTACTCAGGAGGCT 28020

Qy      28021 GAGGCAGGATTCCTCAAGCCCAGGAGTTCAAGGCTTCCGTGAGCTATGATGGCACAACTG 28080
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Db      28021 GAGGCAGGATTCCTCAAGCCCAGGAGTTCAAGGCTTCCGTGAGCTATGATGGCACAACTG 28080

Qy      28081 CACTCCATCTTGGGTGACAGAGCAAGGTCCTATCTCTGGAGAAAAAAAAAAAAAAGAAGGC 28140
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Db      28081 CACTCCATCTTGGGTGACAGAGCAAGGTCCTATCTCTGGAGAAAAAAAAAAAAAAGAAGGC 28140

Qy      28141 ATTTCTTAGGAGAGTTCTTCTCTGTAGAGTCCTAAGGGTTCCATGGAACTCCTTAAAAGC 28200
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Db      28141 ATTTCTTAGGAGAGTTCTTCTCTGTAGAGTCCTAAGGGTTCCATGGAACTCCTTAAAAGC 28200

Qy      28201 ATCAGAGTATGTGAGTGCAATGGGAGGAAGCATTTAGCCAGAGCAGTTGTGCTCCCATTG 28260
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Db      28201 ATCAGAGTATGTGAGTGCAATGGGAGGAAGCATTTAGCCAGAGCAGTTGTGCTCCCATTG 28260

Qy      28261 CATATTAATTTTTAAAAAACAAAGCTATAAAAAAAAAGTTGAAAACTACTACGTTAGCATC 28320
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Db      28261 CATATTAATTTTTAAAAAACAAAGCTATAAAAAAAAGTTGAAAACTACTACGTTAGCATC 28320

Qy      28321 AGCCTGACATTTAATGGCCTCGTAAATCAAACCTTAATTGACTTTTTAGCCAGTTATGCT 28380
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Db      28321 AGCCTGACATTTAATGGCCTCGTAAATCAAACCTTAATTGACTTTTTAGCCAGTTATGCT 28380

Qy      28381 ACTAGCCAACTACAGACAACACACTTTTTAACCAAATTAGACTAATAGTTGTCATCAGTG 28440
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Db      28381 ACTAGCCAACTACAGACAACACACTTTTTAACCAAATTAGACTAATAGTTGTCATCAGTG 28440

Qy      28441 GAAATCAAGTTTGCCATTCTTCCATGCCTTTGCTCACACCATTACCTTTTCTGGAATGTC 28500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28441 GAAATCAAGTTTGCCATTCTTCCATGCCTTTGCTCACACCATTACCTTTTCTGGAATGTC 28500

Qy      28501 CTGTACTCATCTTCCTGTGTTGAACTCTATACCCAACTTTAAAAACCTAGCTCAAAGTTC 28560
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Db      28501 CTGTACTCATCTTCCTGTGTTGAACTCTATACCCAACTTTAAAAACCTAGCTCAAAGTTC 28560

Qy      28561 AACACTTCCATTCCATTTCAAAAAGAGCTTTCCTCTTCCTTAAAGTTTAAGAACTCATTT 28620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28561 AACACTTCCATTCCATTTCAAAAAGAGCTTTCCTCTTCCTTAAAGTTTAAGAACTCATTT 28620

Qy      28621 TCATGAATCTTTTTGGCATTTATTGCACACATGCTTGCTTTGTGTTATTTGTGTTCAGCC 28680
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Db      28621 TCATGAATCTTTTTGGCATTTATTGCACACATGCTTGCTTTGTGTTATTTGTGTTCAGCC 28680

Qy      28681 TCATATGCCCCCAAGGTGTTTTAGACTCCTTAACGGCAAAAATGATGCTCTAAACACCTT 28740
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Db      28681 TCATATGCCCCCAAGGTGTTTTAGACTCCTTAACGGCAAAAATGATGCTCTAAACACCTT 28740

Qy      28741 TCTATCTTTCATAGTGTCTTAGTCTGTTTGTGTTGCTATAAAGGAATACCTGAGGCTGGG 28800
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Db      28741 TCTATCTTTCATAGTGTCTTAGTCTGTTTGTGTTGCTATAAAGGAATACCTGAGGCTGGG 28800

Qy      28801 GAATTTATTTAAAAAAGAGGTTTATTTGGCTCACAGTTCTGCAGCTATATAAGAAGCATA 28860
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Db      28801 GAATTTATTTAAAAAAGAGGTTTATTTGGCTCACAGTTCTGCAGCTATATAAGAAGCATA 28860

Qy      28861 GTGTCAGCATCTGCTTCAGGTGAGGGCTTCAGGAAGTTTCCACCCATGGTAGAAGGCAAA 28920
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Db      28861 GTGTCAGCATCTGCTTCAGGTGAGGGCTTCAGGAAGTTTCCACCCATGGTAGAAGGCAAA 28920

Qy      28921 GGGGAGCAGGCATCACATATCAAGAGAGGAGGAAAAAAAGGAAGGAAGAAAGGAGGGTGC 28980
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Db      28921 GGGGAGCAGGCATCACATATCAAGAGAGGAGGAAAAAAAGGAAGGAAGAAAGGAGGGTGC 28980

Qy      28981 CATTCTCTTTCAACAATCAGTTCTTGTGGGAACTAATGGGACAAGAGGCTGGGCACGGTG 29040
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Db      28981 CATTCTCTTTCAACAATCAGTTCTTGTGGGAACTAATGGGACAAGAGGCTGGGCACGGTG 29040

Qy      29041 GCTCATGCCTGTAATCCCAGCCCTTTGGGAGACCAAGGTGGGTGGATCACCTGAAGTCAG 29100
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Db      29041 GCTCATGCCTGTAATCCCAGCCCTTTGGGAGACCAAGGTGGGTGGATCACCTGAAGTCAG 29100

Qy      29101 AAGCCTGAGACCAGCCTGGCCAATGTGGTGAAACTCCGTCTCTACTAAAAATACAAAAAT 29160
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Db      29101 AAGCCTGAGACCAGCCTGGCCAATGTGGTGAAACTCCGTCTCTACTAAAAATACAAAAAT 29160

Qy      29161 TAGCTGGGCCTGGTGGCGTGTACCTGTAGTCCCAGATACTCAGGAGGCTGAGGTAGGATA 29220
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Db      29161 TAGCTGGGCCTGGTGGCGTGTACCTGTAGTCCCAGATACTCAGGAGGCTGAGGTAGGATA 29220

Qy      29221 ATCACTTGAACCCGGAAGACAGAGGTTGCAGTGAGCTTGTGCCACTGCACTCCAGCCGGG 29280
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Db      29221 ATCACTTGAACCCGGAAGACAGAGGTTGCAGTGAGCTTGTGCCACTGCACTCCAGCCGGG 29280

Qy      29281 GCAACAGAGTGAGACGGTCTCAAAAAATTTTAAAAACTTTAAAAATAATAGAGCAAGAAA 29340
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Db      29281 GCAACAGAGTGAGACGGTCTCAAAAAATTTTAAAAACTTTAAAAATAATAGAGCAAGAAA 29340

Qy      29341 GCACCAAGTTATTCAGGAGGGATCCACCCCCAATGACTCAAATACCTCCCACCAGGCCTC 29400
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Db      29341 GCACCAAGTTATTCAGGAGGGATCCACCCCCAATGACTCAAATACCTCCCACCAGGCCTC 29400

Qy      29401 ACTTCCAACACTGGGGATCAATTTCCGTATGAGATTTGGAGGAGACAAATATCCAAACTA 29460
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Db      29401 ACTTCCAACACTGGGGATCAATTTCCGTATGAGATTTGGAGGAGACAAATATCCAAACTA 29460

Qy      29461 TATCACATAGTAATGAACATAGTACCTTATCTATAGAAAGCAATGGCTAGACAACTGTTG 29520
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Db      29461 TATCACATAGTAATGAACATAGTACCTTATCTATAGAAAGCAATGGCTAGACAACTGTTG 29520

Qy      29521 AATGGCTAACCAAATCTGCTTTCCTATGGTCTCGCTCTAGAGGGGGTCAGTATGAGTTTC 29580
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Db      29521 AATGGCTAACCAAATCTGCTTTCCTATGGTCTCGCTCTAGAGGGGGTCAGTATGAGTTTC 29580

Qy      29581 TGTCAAAAGGAGAAAAAAAAAATGTATAGTCAGTTTTGTGTGTGTGTGTGTTCATGTAAAA 29640
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Db      29581 TGTCAAAAGGAGAAAAAAAAAATGTATAGTCAGTTTTGTGTGTGTGTGTGTTCATGTAAAA 29640

Qy      29641 GAGATCAAGAGAAAAGAACAAGAGAAATCATGAAAAGGAGGGGGAATATAAGAATAATAC 29700
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Db      29641 GAGATCAAGAGAAAAGAACAAGAGAAATCATGAAAAGGAGGGGGAATATAAGAATAATAC 29700

Qy      29701 ATAGAAAAAAGCAAATTATCTTGTTTATCAGTAATACCCAAGGGGGTAGAAATGGTAAGT 29760
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Db      29701 ATAGAAAAAAGCAAATTATCTTGTTTATCAGTAATACCCAAGGGGGTAGAAATGGTAAGT 29760

Qy      29761 AATAATCCTTCTTCACTTTGTCTGTAGTTCACTTTTTTGCACCTTTATTTTGATGAATTC 29820
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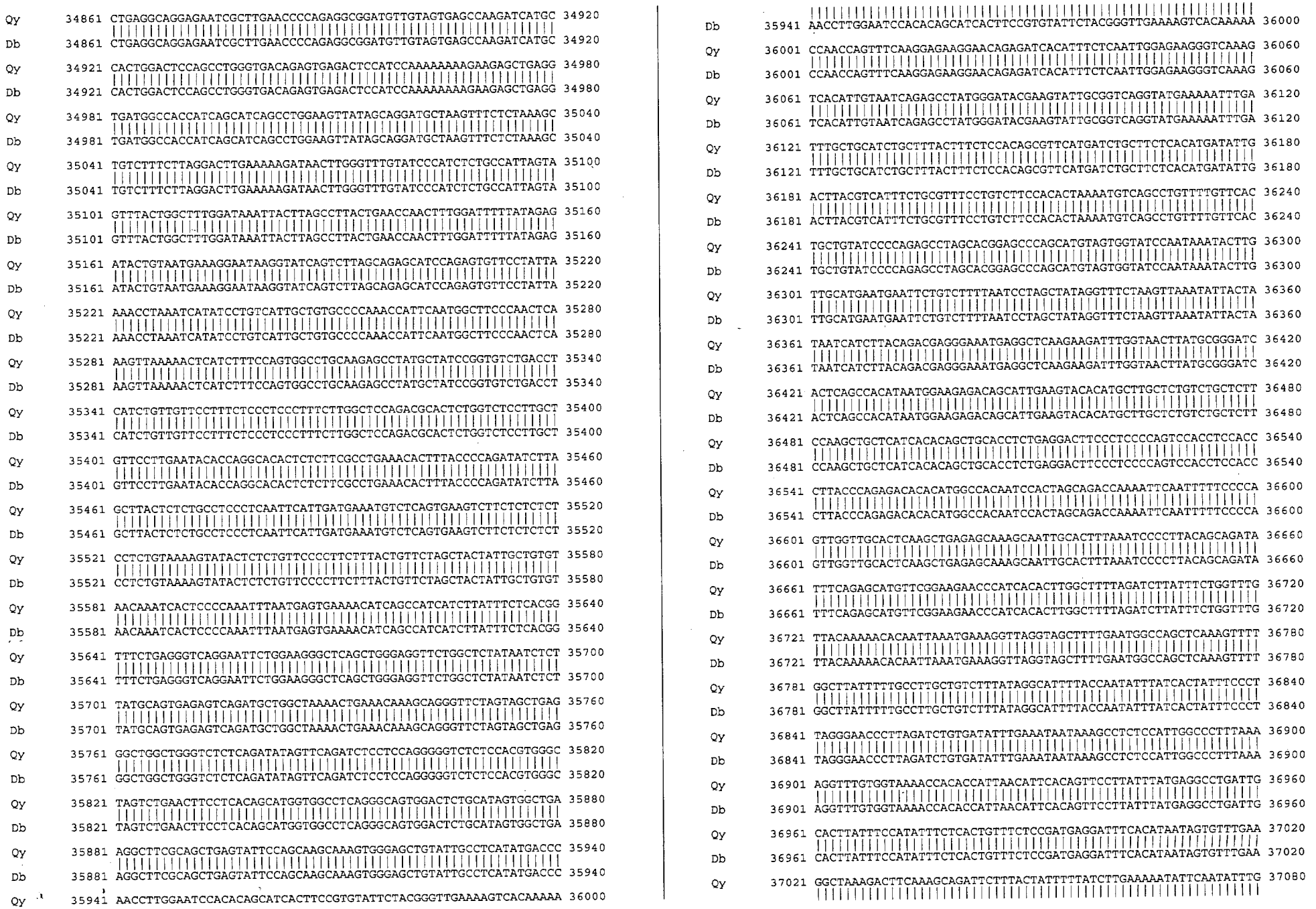
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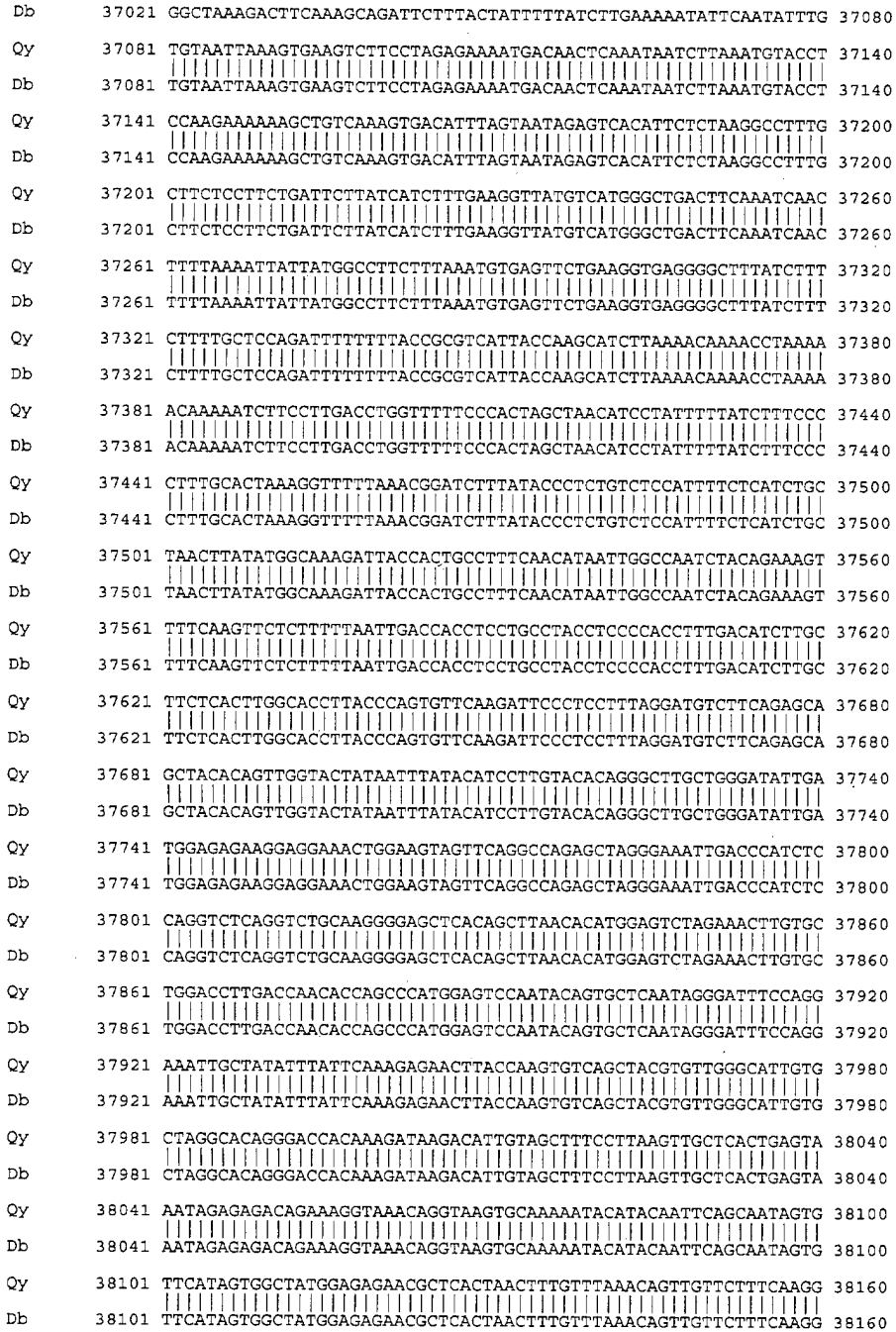
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  AUTHORS   Barry,A.E., Bateman,M., Howman,E.V., Cancilla,M.R., Tainton,K.M.,
            Irvine,D.V., Saffery,R. and Choo,K.H.
  TITLE     The 10q25 neocentromere and its inactive progenitor have identical
            primary nucleotide sequence: further evidence for epigenetic
            modification
  JOURNAL   Genome Res. 10 (6), 832-838 (2000)
  MEDLINE   20314874
   PUBMED   10854414
REFERENCE   2  (bases 1 to 80622)
  AUTHORS   Barry,A.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JAN-2000) Chromosome Research Unit, The Murdoch
            Institute, 10th Floor, Royal Childrens Hospital, Flemington Rd.,
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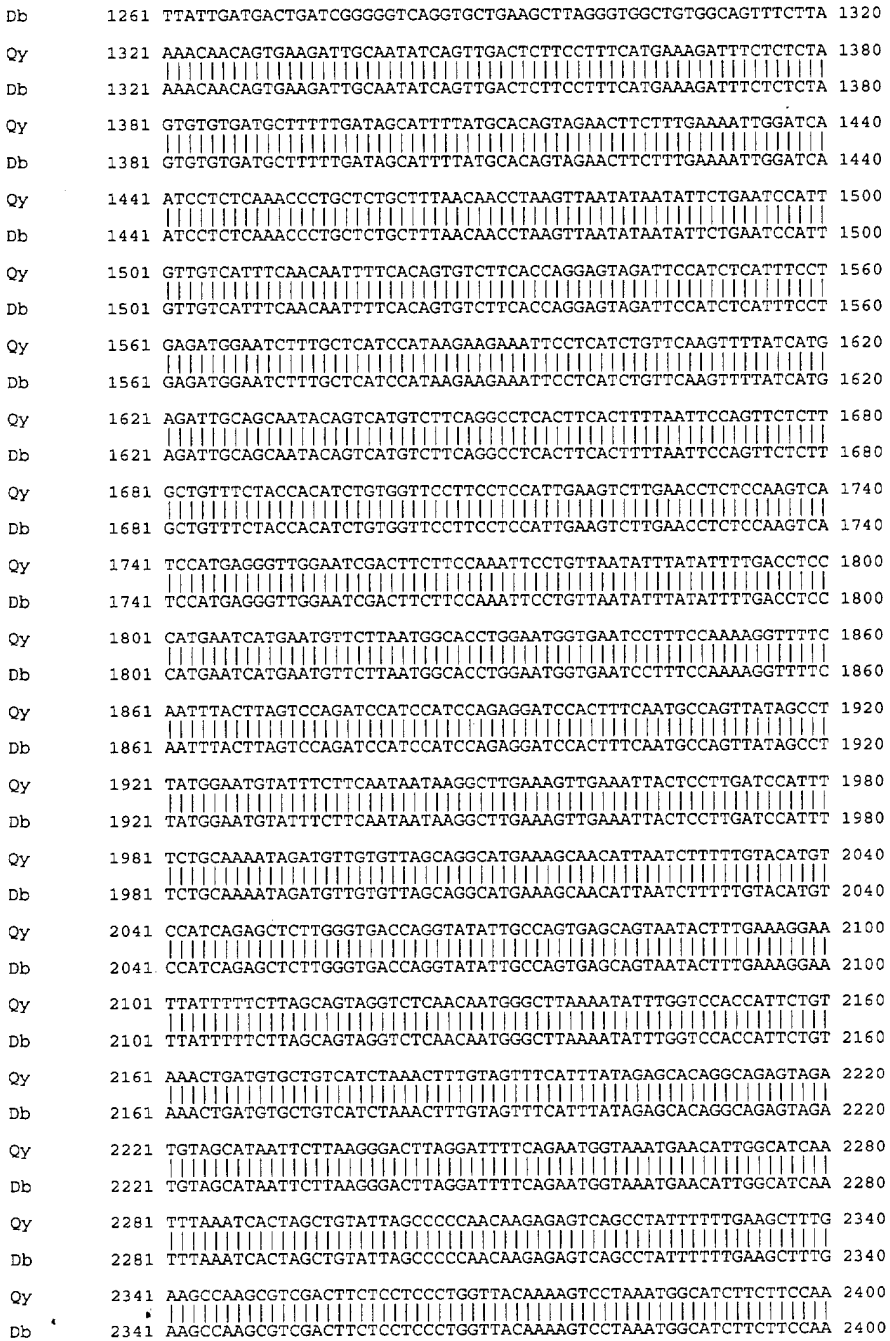
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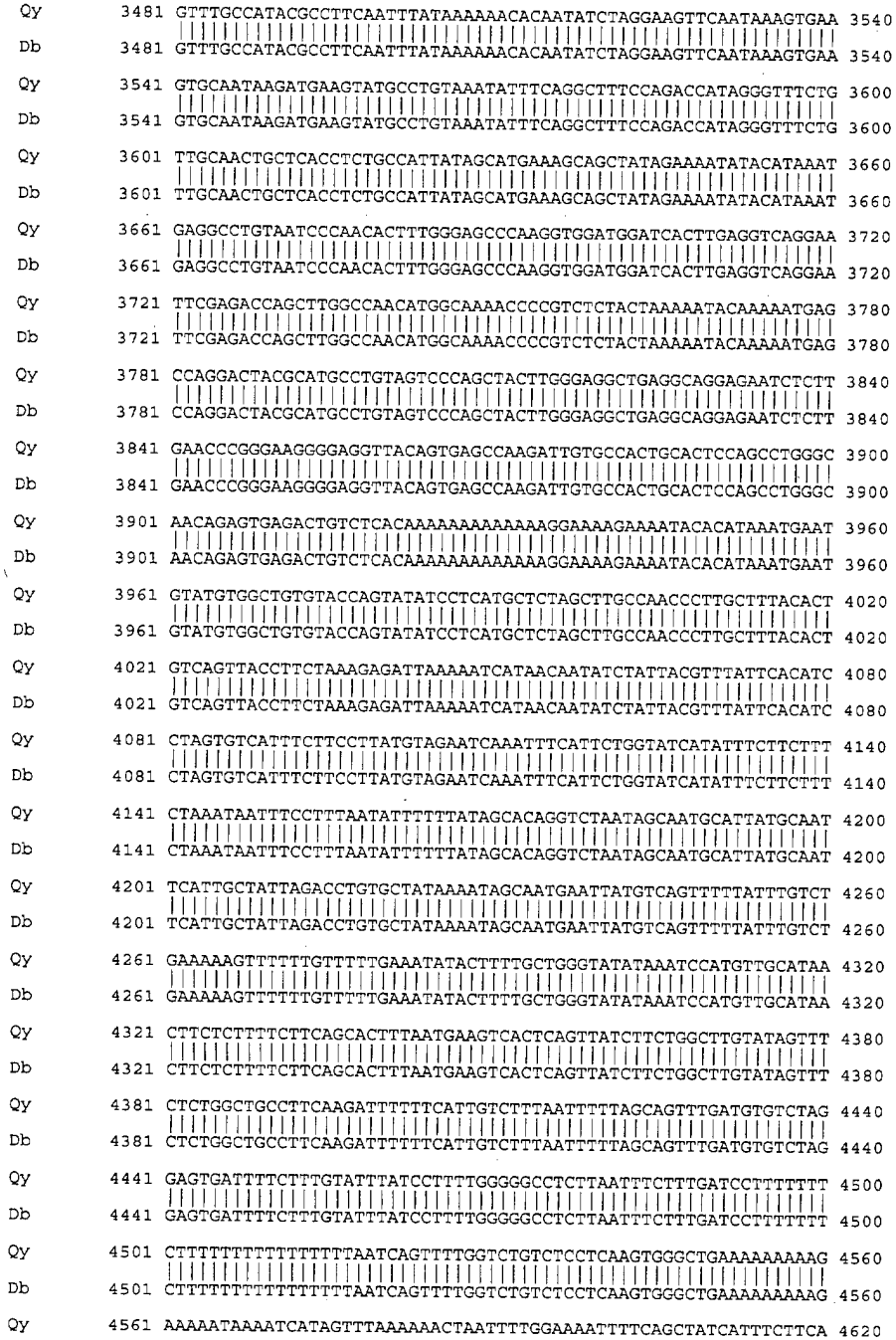
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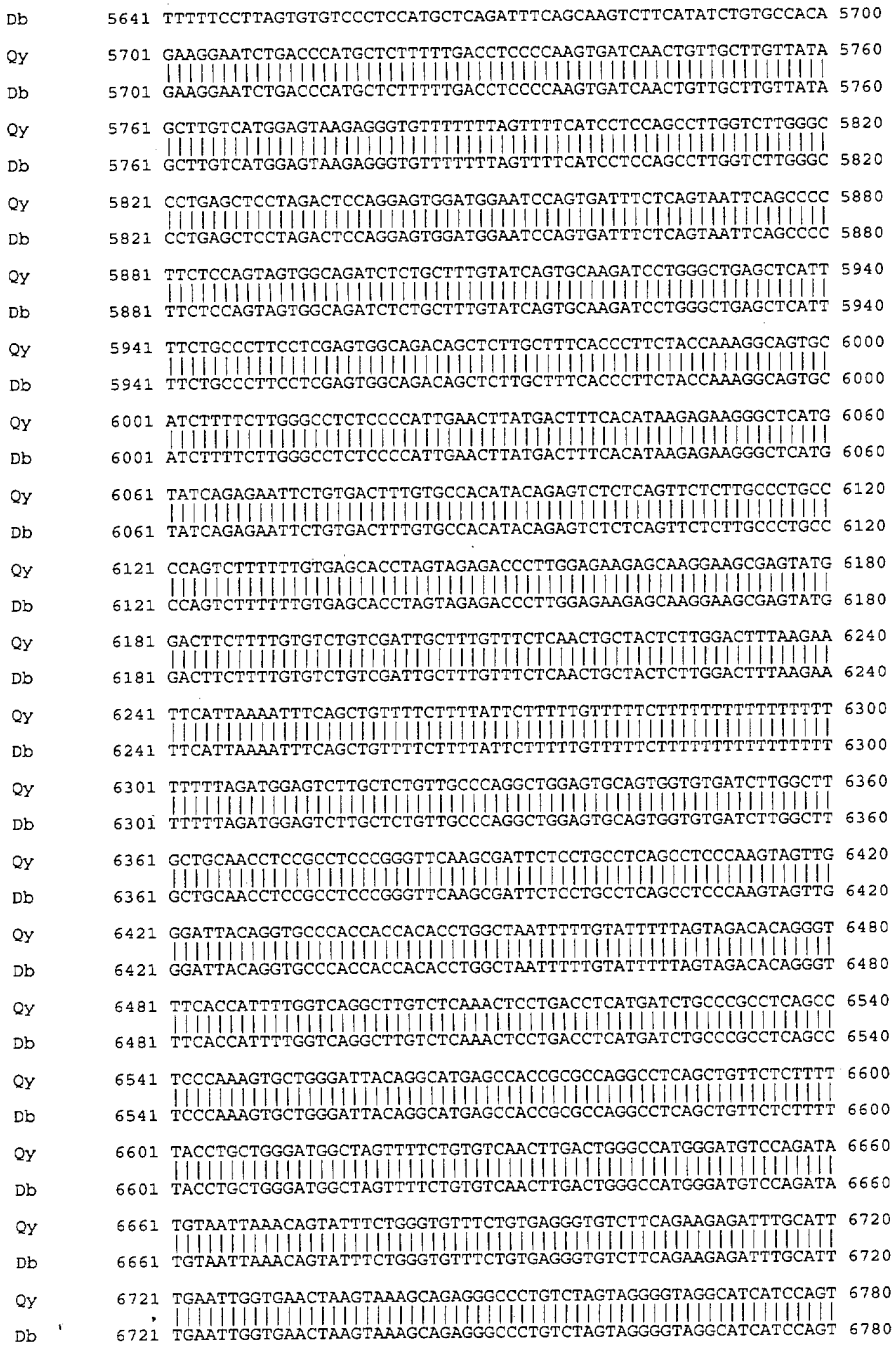
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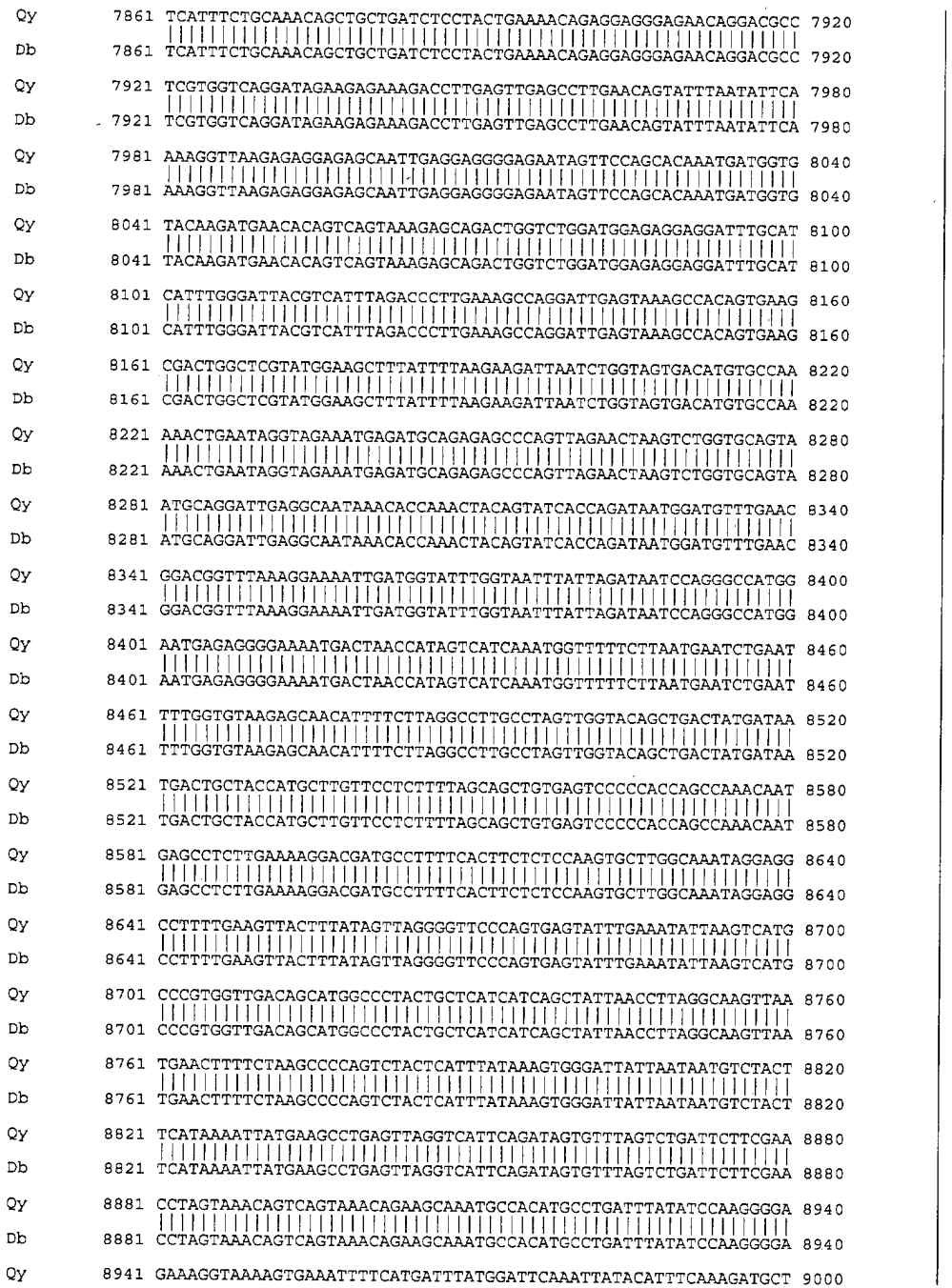
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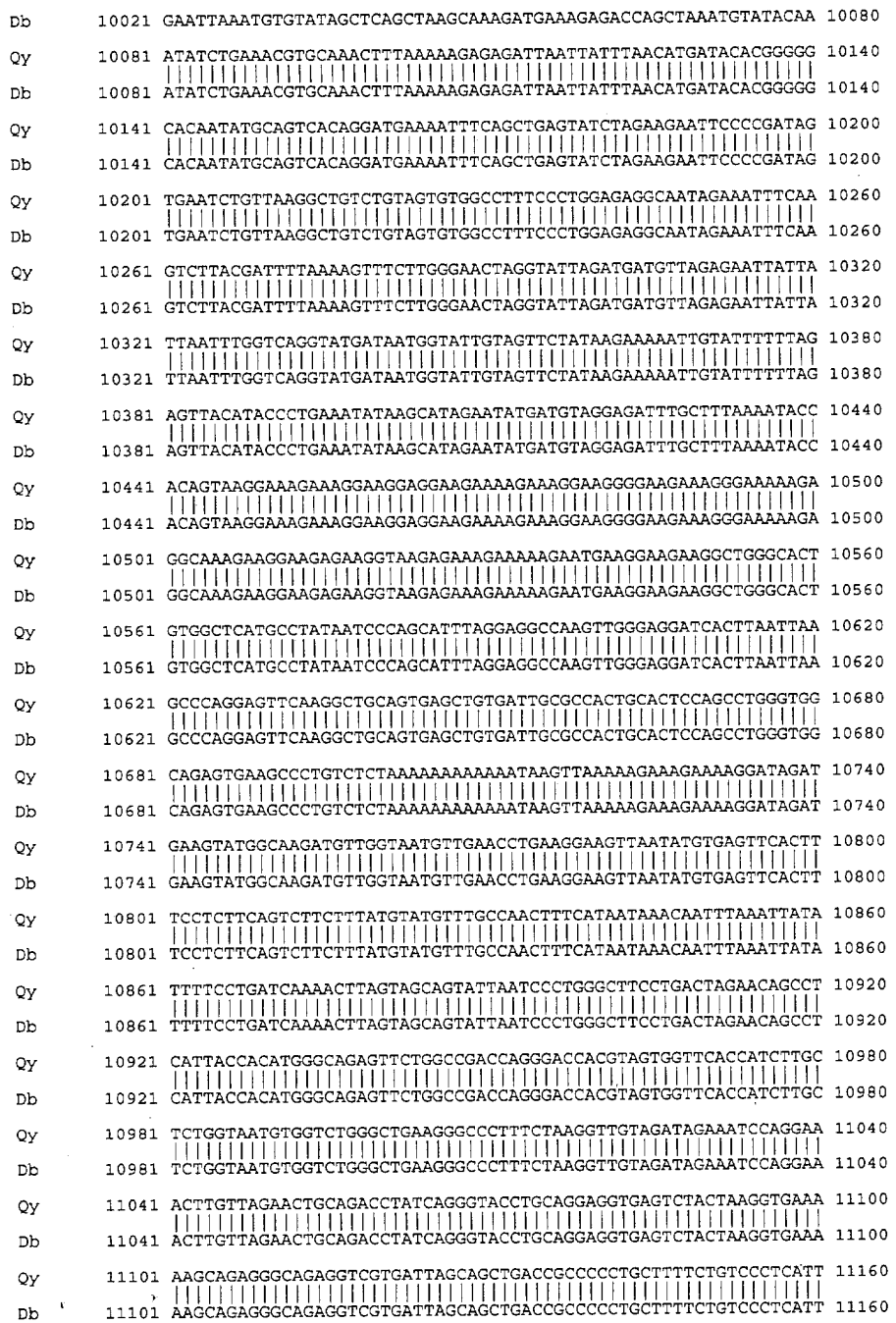
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Db      13021 GTCCTTGAATGGGGAAATATTTCCCTTCATTCCTGTGTTTTAGGGACAGAAAGATGAGTA 13080

Qy      13081 ATGCAGTGATACATGCTGGAAATGTTTATTCCACTACCCGAAGCTGCCTCTCAACTTAAC 13140
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Qy      13141 AATCCATGAAAGAAACAAGATGGTATATAACTTTTTCTAATTTGTGATGCCTTTGTTTAT 13200
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Qy      13201 TTGTTTCCGGTTAAAAGAGGAGGTGGCATTGAATTGTTTGTTTGGTTTGGTTTCTTCTTC 13260
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Qy      13261 AATAAGAAGCATCTTAATATAACTAGACTGGACATCTGTCCCATTTTCAAAAATTACAAG 13320
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Qy      13321 TTTCGATCATTGCTAAATTGTACAGATCCCAATCTGTCTGCTCTGCATACATTTGCATTT 13380
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Qy      13381 ATAAAAGCAGAAGCAGACTAGCAGTCTTTCTAATGCAATCCCCCAAATGCATGAAGTATT 13440
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Qy      13441 AGATTGCTTCTCCCTATTGGTTCATGCATTGCTAAAGGCTTAAAAGGATCATTGATTTTA 13500
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Qy      13501 ATTATTTAATGTGTACAGCAGGCTGAGCTTCCTTTCTTTTTTAAGGGAAGAACCTTCAGG 13560
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Db      13501 ATTATTTAATGTGTACAGCAGGCTGAGCTTCCTTTCTTTTTTAAGGGAAGAACCTTCAGG 13560

Qy      13561 GGCATTGCTTTAGTTTTTTAATGTTAAATCTCATTTTTCTTTGAAAATAAGAAGTTAAAG 13620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13561 GGCATTGCTTTAGTTTTTTAATGTTAAATCTCATTTTTCTTTGAAAATAAGAAGTTAAAG 13620

Qy      13621 CTGTATTCACACAAGCTCTCAAAGTGCCAGATTTTCATTGTGTTTTTAAACCATCTAGGA 13680
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Qy      13681 AATGTTTGATTCTAATGAAACATTACTGCTGAAAATTGGGCTGAAATTGCTGGGCTGGAA 13740
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Qy      13801 TGACCCGATATAGATGAAGCGAAGAGACAAGGAGCAATCCCATGTGTAATAGAAAAAGGC 13860
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Qy      13861 AGCCTGAATTGTTGTTGCTGTTTTTGAAATTTAAGCTGGTTTTCGATTAAATTCAGTAAA 13920
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Qy      13981 GTTTTTTTTTTTTTTGATGGTTTACATTTTCCCCATGGGAAGCAGCTATGTCATGTCGGC 14040
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Qy      14041 ATGATTCATCATGGTAACATCTCGGGTTATTTTGGTTTGTGTTATGTTCAGAAAGCGGAA 14100
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Qy      14101 TGCCAAAAATAAAGAGTGGTTTGTGATGTCTAGTGTGTCTTCCTTTAACAAATCAAAGGC 14160
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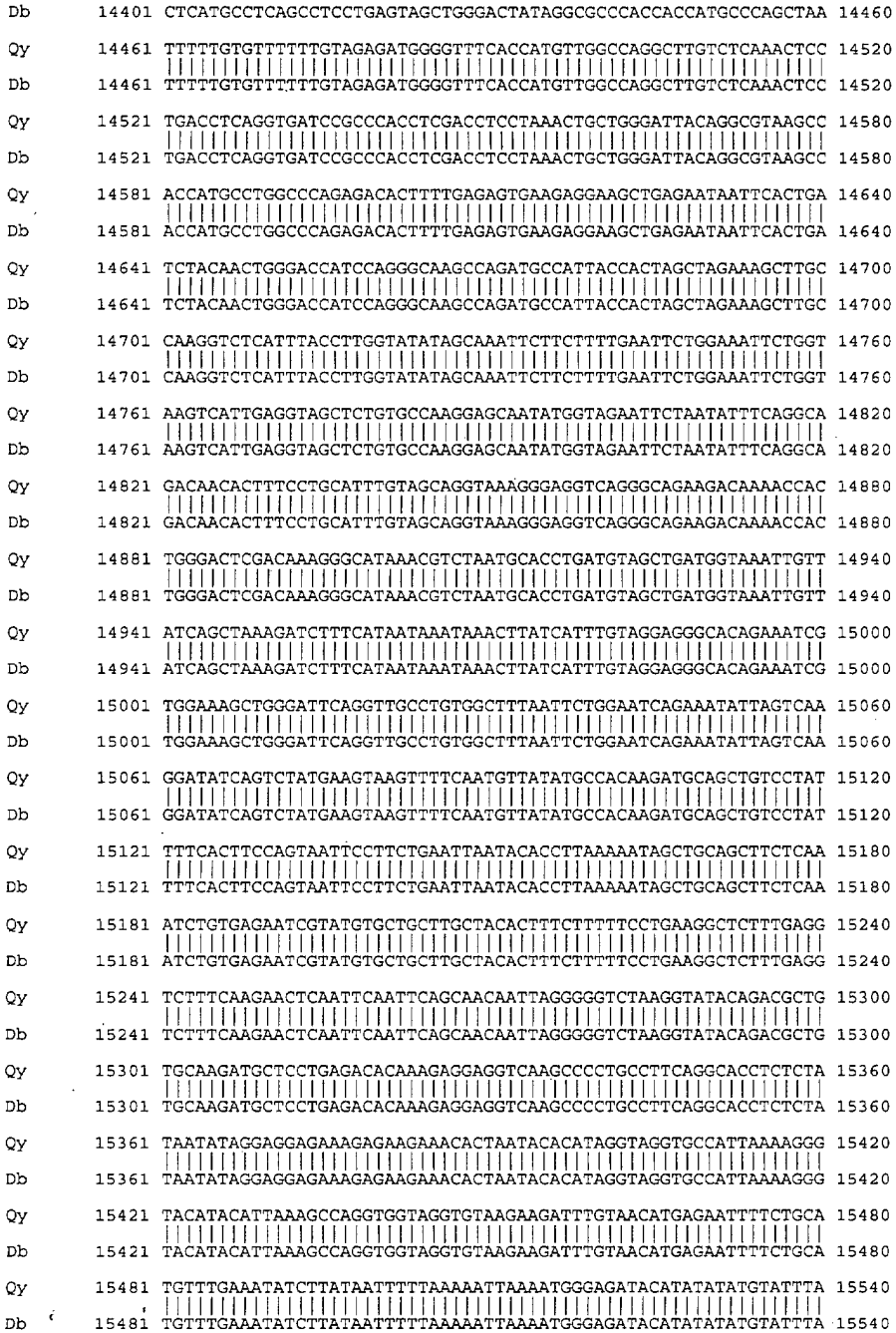
Qy      14161 TTTTATTTAATCCACTTAATGGGACACTGCAGAAATTTAAAAAATGGAAGTCCCATCCAC 14220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14161 TTTTATTTAATCCACTTAATGGGACACTGCAGAAATTTAAAAAATGGAAGTCCCATCCAC 14220

Qy      14221 AGAAGGCAGGTACTATGATGTAAAAAGTTTAGGTGGGGGATTAATAGAGTGATCATATAA 14280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14221 AGAAGGCAGGTACTATGATGTAAAAAGTTTAGGTGGGGGATTAATAGAGTGATCATATAA 14280

Qy      14281 TTTATGAGCTAAACCGGAGGCACTTTTTTTTTTGAGATCGAGTCTCACTGTTGCCTAGGC 14340
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Db      14281 TTTATGAGCTAAACCGGAGGCACTTTTTTTTTTGAGATCGAGTCTCACTGTTGCCTAGGC 14340

Qy      14341 TGGAGTGCAGTGACGTGATCACAGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGATT 14400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14341 TGGAGTGCAGTGACGTGATCACAGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGATT 14400

Qy      14401 CTCATGCCTCAGCCTCCTGAGTAGCTGGGACTATAGGCGCCCACCACCATGCCCAGCTAA 14460
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Db 14401 CTCATGCCTCAGCCTCCTGAGTAGCTGGGACTATAGGCGCCCACCACCATGCCCAGCTAA 14460
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Qy 14581 ACCATGCCTGGCCCAGAGACACTTTTGAGAGTGAAGAGGAAGCTGAGAATAATTCACTGA 14640
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Qy      16594 TATCCGATGGATGGCCCTTAAGGTGAGCTCAAGGCTTAAGGGAGAGATAGGGGCTGATGA 16653
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Qy      16714 TCCAGGGAGAGCGTAGATAAAGAAGCTAAATGGCTTCTGGGTCCTTAGTCATTCAAAATC 16773
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Qy      16774 GGACCTCTGAGGCAGGAGGAAAGCCCAGAAAGAGTAGATTCCTGGGACTCACGGGATAAA 16833
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Qy      17614 GCACCTGTAATCCCAGCTGTTCAGTTGGCTGAGTCAGGAGAATAGCCTGGATCCGGGAAG 17673
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Qy      17674 TGGAGGTTGTAGTAAGCCAAGATTGCGCCACTGCATGCCAGCCTGGGCGACAGAGCAAGA 17733
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Db      17701 TGGAGGTTGTAGTAAGCCAAGATTGCGCCACTGCATGCCAGCCTGGGCGACAGAGCAAGA 17760

Qy      17734 CTTTTCTTAAAACAAACAAACAAAAAAGAAAAAAGAAAAGGAAAGAAGAAAGAGACAAAG 17793
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Db      17761 CTTTTCTTAAAACAAACAAACAAAAAAGAAAAAAGAAAAGGAAAGAAGAAAGAGACAAAG 17820

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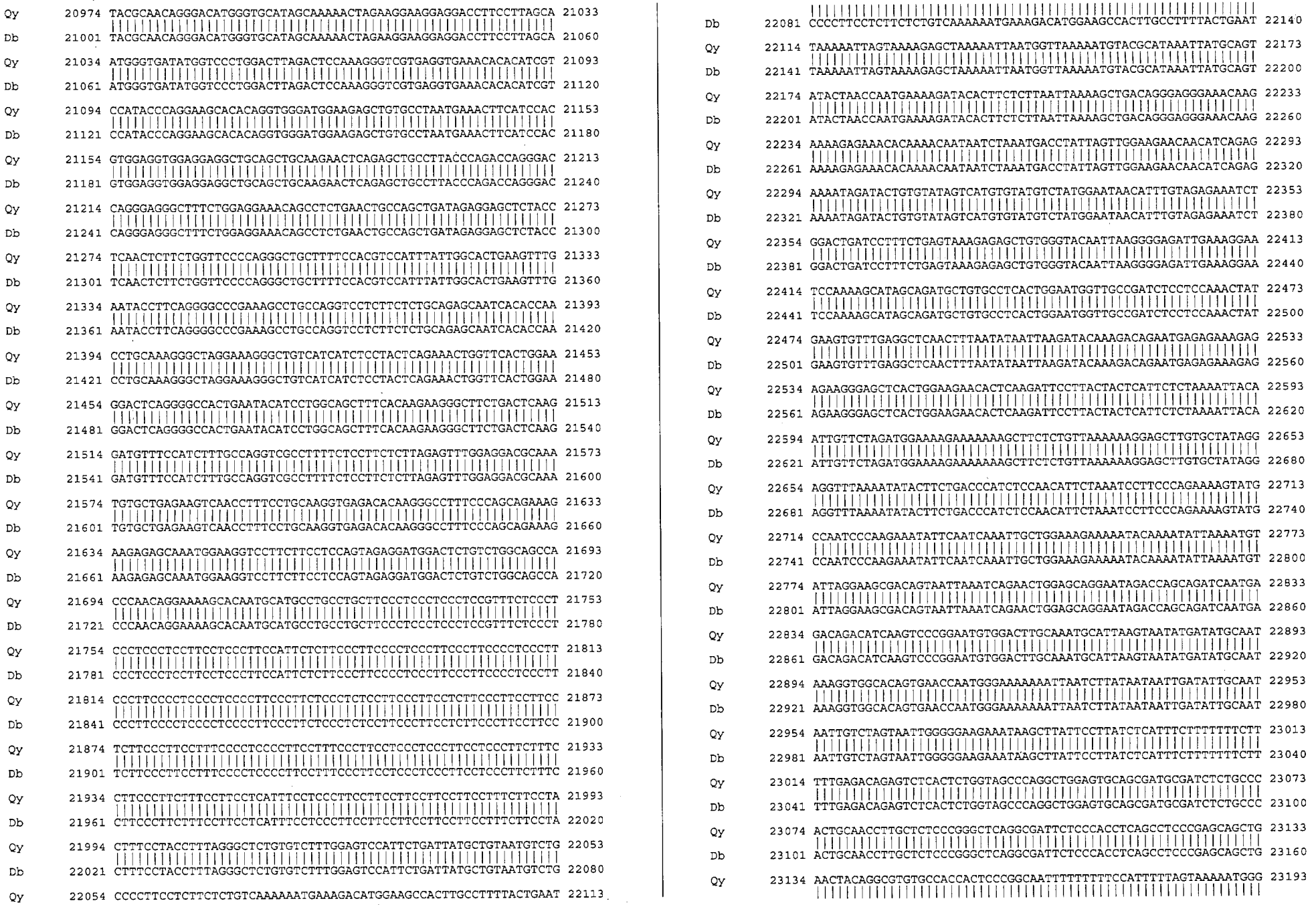
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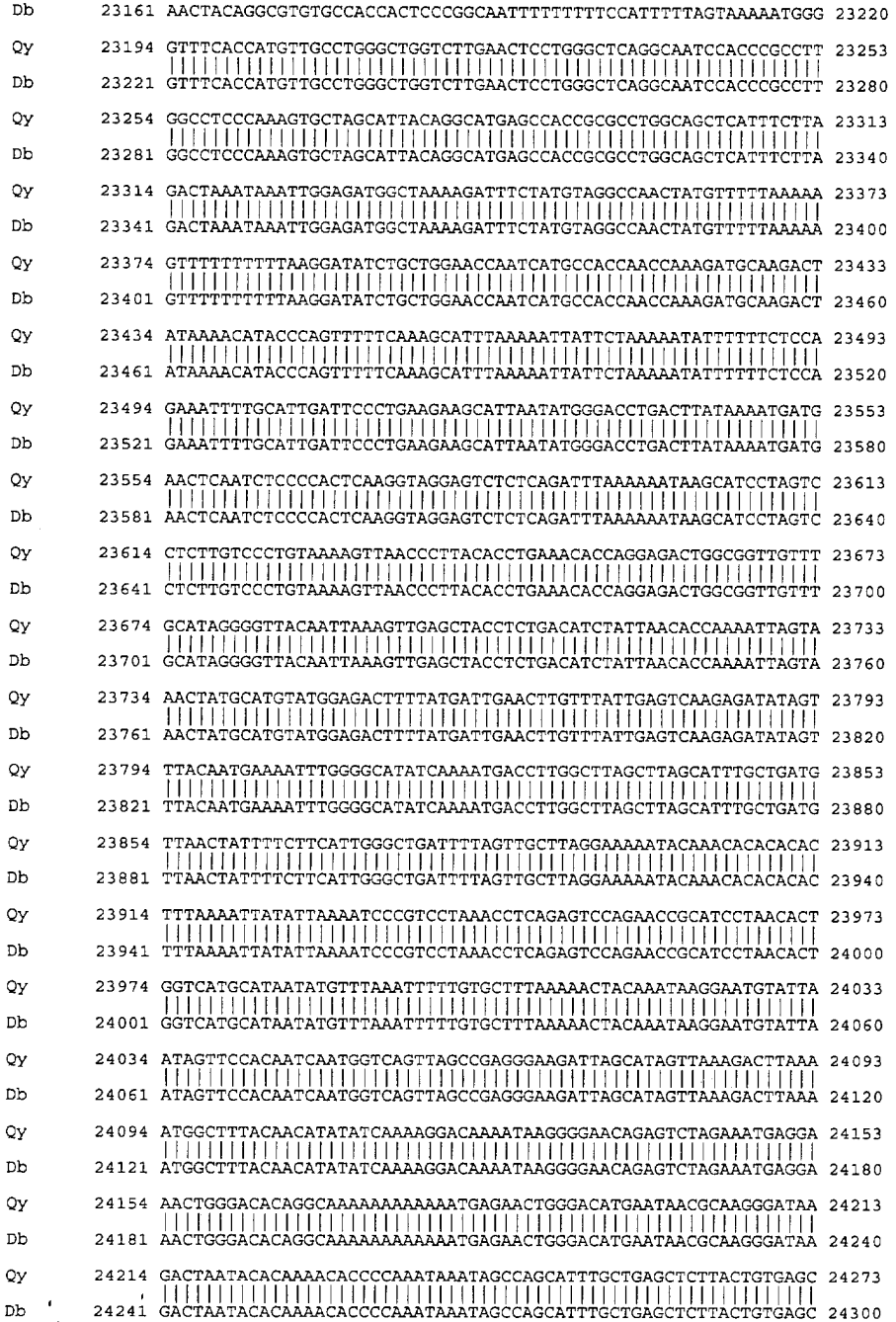
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Db 24661 AAATCCCACTTCTTCTCTGAGTGGTCCATACAGTTTTACTCTACTTGCTTACAGAATGAA 24720
Qy 24694 AATAGCTGGAGTTCAGGTGCGCTTTCAATGCCCTGTTGTCAGGATTGGGCTTTTCAAGTT 24753
Db 24721 AATAGCTGGAGTTCAGGTGCGCTTTCAATGCCCTGTTGTCAGGATTGGGCTTTTCAAGTT 24780
Qy 24754 TATTTTTTGTTGTTGTTTTTAATAGACTGTACTTTTTAGAAAATTTTTAGATTTACAGAA 24813
Db 24781 TATTTTTTGTTGTTGTTTTTAATAGACTGTACTTTTTAGAAAATTTTTAGATTTACAGAA 24840
Qy 24814 AGATTGAGAGGATAGTACAGAGAGTTCCCGTATACCTCACACCCAGTTTCTGCAATTATT 24873
Db 24841 AGATTGAGAGGATAGTACAGAGAGTTCCCGTATACCTCACACCCAGTTTCTGCAATTATT 24900
Qy 24874 AACCTCTTACATTCATGCGGTACATTTGTTACAATTAATGAGCCAGGGCCGGCCGGGCAC 24933
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Qy 24934 AGTGGTTCAGGCCCCTAATCCCAGCACTTTGGGAGGCAGAGGCAAGCGAATCACTTGAGG 24993
Db 24961 AGTGGTTCAGGCCCCTAATCCCAGCACTTTGGGAGGCAGAGGCAAGCGAATCACTTGAGG 25020
Qy 24994 TCAGGAGTTCGAGACTAGCCTGACCAACATGGTAAACCCTTTCTGTACTAAAAATACAAA 25053
Db 25021 TCAGGAGTTCGAGACTAGCCTGACCAACATGGTAAACCCTTTCTGTACTAAAAATACAAA 25080
Qy 25054 AAATTAGCCAGGCATGGTGCTGGTTGCCTGTATTCCCAGATACTCAGGAGGCTGAGGCAC 25113
Db 25081 AAATTAGCCAGGCATGGTGCTGGTTGCCTGTATTCCCAGATACTCAGGAGGCTGAGGCAC 25140
Qy 25114 AAGAATTGCTTGAACCAGGGAGGCGGAGGTTGCAGTAAGCCGAGATCGTGCCACTGCACT 25173
Db 25141 AAGAATTGCTTGAACCAGGGAGGCGGAGGTTGCAGTAAGCCGAGATCGTGCCACTGCACT 25200
Qy 25174 CCAGCCTGGGCAACAGAGCGAGACTCCATCAAAAAAAAAAAAAAAAAAAAAAAGAAGGAAG 25233
Db 25201 CCAGCCTGGGCAACAGAGCGAGACTCCATCAAAAAAAAAAAAAAAAAAAAAAGAAGGAAG 25260
Qy 25234 GAAGGAAGGAAAATTAATGAGCCAATATTGAGACATTATTATTACTAAAGTCCATGCTTT 25293
Db 25261 GAAGGAAGGAAAATTAATGAGCCAATATTGAGACATTATTATTACTAAAGTCCATGCTTT 25320
Qy 25294 ATGCAGATTTTCTTAGTTTTTACCTGCTGTCATTTTTCAGTTCCAGGAATGCATTCAGGA 25353
Db 25321 ATGCAGATTTTCTTAGTTTTTACCTGCTGTCATTTTTCAGTTCCAGGAATGCATTCAGGA 25380

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Qy      25354 TGCCATACCACATTTAGTTCTCATATCTGCTTAGGCTCCTCTTGGCTAGACTGAGTTTTA 25413
Db      25381 TGCCATACCACATTTAGTTCTCATATCTGCTTAGGCTCCTCTTGGCTAGACTGAGTTTTA 25440

Qy      25414 ATCTACTTTCTGCAGAGCCTGAGAACTTTAGCATAATTTCCTTGGAAATTACAGCTCAAT 25473
Db      25441 ATCTACTTTCTGCAGAGCCTGAGAACTTTAGCATAATTTCCTTGGAAATTACAGCTCAAT 25500

Qy      25474 ATTTTCAAGCACTTATACAAACAGCCTAATGTTACGTTGGCCCATAACAGTGTTTCAAGG 25533
Db      25501 ATTTTCAAGCACTTATACAAACAGCCTAATGTTACGTTGGCCCATAACAGTGTTTCAAGG 25560

Qy      25534 TAATAAACTTCTTTGTTTTCTGTGCCGATTGAAAGAACTGCTGCTTAGCCTCCTGCCAGA 25593
Db      25561 TAATAAACTTCTTTGTTTTCTGTGCCGATTGAAAGAACTGCTGCTTAGCCTCCTGCCAGA 25620

Qy      25594 TGATGAACTGGGTACACACGAGCATTTTTCCAGGTAAAGCATATTTCGTGCGACTTCTTA 25653
Db      25621 TGATGAACTGGGTACACACGAGCATTTTTCCAGGTAAAGCATATTTCGTGCGACTTCTTA 25680

Qy      25654 AGCTGCAGCCTTATATGCAATAATTGTCCATTTACAAGACTTATGTTCGAATTTCAGGCA 25713
Db      25681 AGCTGCAGCCTTATATGCAATAATTGTCCATTTACAAGACTTATGTTCGAATTTCAGGCA 25740

Qy      25714 CTCTGTTTTCACTAACCATATCCTTCAACTTTGATAAGTACTGCTTTAATCAACTCAGAA 25773
Db      25741 CTCTGTTTTCACTAACCATATCCTTCAACTTTGATAAGTACTGCTTTAATCAACTCAGAA 25800

Qy      25774 AATTTAACTTGACTAATTTTTTTTTCACCATCAGTTTTTTTTCTGTTGACTCTTTCTCCTT 25833
Db      25801 AATTTAACTTGACTAATTTTTTTTTCACCATCAGTTTTTTTTCTGTTGACTCTTTCTCCTT 25860

Qy      25834 TTTCTGTTTGCCCAGAAACATGCTCAGGATTCTCTCAGGCTTTAAAAAATGAAAAAATGT 25893
Db      25861 TTTCTGTTTGCCCAGAAACATGCTCAGGATTCTCTCAGGCTTTAAAAAATGAAAAAATGT 25920

Qy      25894 TTCCTGCAATCTAGTTACTCCTTGATTCTCTTGTTCTGTTTATCGCTGGAATTCTTGAAA 25953
Db      25921 TTCCTGCAATCTAGTTACTCCTTGATTCTCTTGTTCTGTTTATCGCTGGAATTCTTGAAA 25980

Qy      25954 GCTTGGTGTATTAGTCTTTTTTCATGCTGCTGATAAAGATATACCTGAGACTGGATAATT 26013
Db      25981 GCTTGGTGTATTAGTCTTTTTTCATGCTGCTGATAAAGATATACCTGAGACTGGATAATT 26040

Qy      26014 TATAAAGAAAAAGAGGTTTAATGGACTCACAGTTCCACGTGGCTGAGGAAGCCTCACAAT 26073
Db      26041 TATAAAGAAAAAGAGGTTTAATGGACTCACAGTTCCACGTGGCTGAGGAAGCCTCACAAT 26100

Qy      26074 CATGGTGGAAGGCAAAAGGCATGTCTTACATGGCAGCAGACAAGAGAGAATGAGAACCAA 26133
Db      26101 CATGGTGGAAGGCAAAAGGCATGTCTTACATGGCAGCAGACAAGAGAGAATGAGAACCAA 26160

Qy      26134 GGGATTTCCCCTTATAAAACCATCAGATCTTGTGAGACTTATTCACTACCACAAGAACAA 26193
Db      26161 GGGATTTCCCCTTATAAAACCATCAGATCTTGTGAGACTTATTCACTACCACAAGAACAA 26220

Qy      26194 TATGGGGTAAACCGCCCCCATGATTCAATTATCTCCCACCGGGGCCCTCCCACAACACGT 26253
Db      26221 TATGGGGTAAACCGCCCCCATGATTCAATTATCTCCCACCGGGGCCCTCCCACAACACGT 26280

Qy      26254 GGGAATTATGGGAGCTACAATTCAAGATGACATTTGGGTGGGGACATGGCCAAACCATAT 26313
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Qy      26314 CACCTGGCCTATAGCATTATTTCCATTTCTTCCCCATCCTTTTATTCCTCAAACCGGTAC 26373
Db      26341 CACCTGGCCTATAGCATTATTTCCATTTCTTCCCCATCCTTTTATTCCTCAAACCGGTAC 26400

Qy      26374 AACCAGACCTCTTTTTTTTTTTTTCTACCTGAAACTGCTCTTTTGAGGGTAGCTGATAAG 26433
Db      26401 AACCAGACCTCTTTTTTTTTTTTTCTACCTGAAACTGCTCTTTTGAGGGTAGCTGATAAG 26460

Qy      26434 TCCAAAATACTGTCACCTTTTCTCAATTCCGTTCCTTCTTATGCCTTTGGAGCAATTGAC 26493

Db      26461 TCCAAAATACTGTCACCTTTTCTCAATTCCGTTCCTTCTTATGCCTTTGGAGCAATTGAC 26520

Qy      26494 TGTGTTGGTTGCCCCCTCCTTTAAAGTGTCTCTCACTTGGTTTTATGACTAATGATGATT 26553
Db      26521 TGTGTTGGTTGCCCCCTCCTTTAAAGTGTCTCTCACTTGGTTTTATGACTAATGATGATT 26580

Qy      26554 TTCTTTTTCCTCTCTAAACATTCCGCTATCTTTTTAGCTTCCCTTCCCCCTCCCATCCCC 26613
Db      26581 TTCTTTTTCCTCTCTAAACATTCCGCTATCTTTTTAGCTTCCCTTCCCCCTCCCATCCCC 26640

Qy      26614 TAAATGTCCTTGTTTCCCAGAATCTGCCTCACCTCTTTGACTTCTCTATGCCCTGTCATT 26673
Db      26641 TAAATGTCCTTGTTTCCCAGAATCTGCCTCACCTCTTTGACTTCTCTATGCCCTGTCATT 26700

Qy      26674 CACTCATGGGTCTTTATTACATTATTGCATCTGTGTCAATAACTCTGGTCTTTCTGTTAA 26733
Db      26701 CACTCATGGGTCTTTATTACATTATTGCATCTGTGTCAATAACTCTGGTCTTTCTGTTAA 26760

Qy      26734 GTTCCAGTCTCCCATTTTCAAATGTCCCCAGACATTTCCAATTGAGTATCTCTCCAATGT 26793
Db      26761 GTTCCAGTCTCCCATTTTCAAATGTCCCCAGACATTTCCAATTGAGTATCTCTCCAATGT 26820

Qy      26794 ATTTAACCTGCTAAATATCTAACACATAATCTTTCCCATCAAATCGTTTCCTCTTAAGCT 26853
Db      26821 ATTTAACCTGCTAAATATCTAACACATAATCTTTCCCATCAAATCGTTTCCTCTTAAGCT 26880

Qy      26854 TTTCGTTATTTCCTATTAGACTCCTGCACTTCTCCCAGGAGCCCAGACTTAAAACCTTGA 26913
Db      26881 TTTCGTTATTTCCTATTAGACTCCTGCACTTCTCCCAGGAGCCCAGACTTAAAACCTTGA 26940

Qy      26914 ATTTCTCACCATAACCTCTCTTTTGTCTCCCATAATCAATTAGTAGCAAGTGTTATCAAT 26973
Db      26941 ATTTCTCACCATAACCTCTCTTTTGTCTCCCATAATCAATTAGTAGCAAGTGTTATCAAT 27000

Qy      26974 GATTACTTGACAATATCTTTTTCTATTTCCCTCCCTGCTATGATCATTCATCTAGCAAGA 27033
Db      27001 GATTACTTGACAATATCTTTTTCTATTTCCCTCCCTGCTATGATCATTCATCTAGCAAGA 27060

Qy      27034 AGAGTTGGCCCTTTGTATCTGTGGTTTCTGCATCCCTGGATTCAACCAACTGTAGATGGA 27093
Db      27061 AGAGTTGGCCCTTTGTATCTGTGGTTTCTGCATCCCTGGATTCAACCAACTGTAGATGGA 27120

Qy      27094 AAATATTTGAAGAAAAAAGCGTCTATACTGAGTATGAAAAAATTTTATTTCTTGTCATTA 27153
Db      27121 AAATATTTGAAGAAAAAAGCGTCTATACTGAGTATGAAAAAATTTTATTTCTTGTCATTA 27180

Qy      27154 TTCCCTAAACAATACAGTATAACAACTACAGCATTTACACTGTAGCGTATAGATCTTATA 27213
Db      27181 TTCCCTAAACAATACAGTATAACAACTACAGCATTTACACTGTAGCGTATAGATCTTATA 27240

Qy      27214 ATCTAGAAATGATTTCAAGTACACCATTATATATAAGGGACTTGAGCATCTGTGAAGTTT 27273
Db      27241 ATCTAGAAATGATTTCAAGTACACCATTATATATAAGGGACTTGAGCATCTGTGAAGTTT 27300

Qy      27274 GGTATTTGTGGGGCATACTGGGACCAATTCCCCCATGGATACAGAGGGACAACTATATTT 27333
Db      27301 GGTATTTGTGGGGCATACTGGGACCAATTCCCCCATGGATACAGAGGGACAACTATATTT 27360

Qy      27334 ACTCAGTGCTTACTAAATACCAGTTGGCCAATGTGTTTTTCTTTTTCTGTTTTCCTGTCT 27393
Db      27361 ACTCAGTGCTTACTAAATACCAGTTGGCCAATGTGTTTTTCTTTTTCTGTTTTCCTGTCT 27420

Qy      27394 TTAGTTTGCCCCTTGCCAATTAATTCAATAGTGCTGCCAATGCCAGGTGTACCTTCAGAA 27453
Db      27421 TTAGTTTGCCCCTTGCCAATTAATTCAATAGTGCTGCCAATGCCAGGTGTACCTTCAGAA 27480

Qy      27454 TATTCTATTCTAATTTTGTCATCTCCAAGCTTAAAAATATTTAATGGGCCAGGCGCAGTG 27513
Db      27481 TATTCTATTCTAATTTTGTCATCTCCAAGCTTAAAAATATTTAATGGGCCAGGCGCAGTG 27540

Qy      27514 GCTCACACTTGTAATCCCAGCATTTTGGGAGGCCAAGGGGGGGTGTATCACTTGAGGTCA 27573
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Db      27541 GCTCACACTTGTAATCCCAGCATTTTGGGAGGCCAAGGGGGGGTGTATCACTTGAGGTCA 27600

Qy      27574 GGAGTTCCAGACCAGCCTGGCCAACATGGCGAAACCCTGTCTCTACAAAAAAGTATAAAA 27633
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Db      27601 GGAGTTCCAGACCAGCCTGGCCAACATGGCGAAACCCTGTCTCTACAAAAAAGTATAAAA 27660

Qy      27634 GTTAACCAGGTGCTGGAGCATTTGCCTGTGGTCCCAGCTACTCAGGAGGCTGAGGCAGGA 27693
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Db      27661 GTTAACCAGGTGCTGGAGCATTTGCCTGTGGTCCCAGCTACTCAGGAGGCTGAGGCAGGA 27720

Qy      27694 AAATCACTTTAATCTGGGAGGTGGAGTTTGCAGTGAGCCAAGATCTCTCCACTGCACTCC 27753
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Db      27721 AAATCACTTTAATCTGGGAGGTGGAGTTTGCAGTGAGCCAAGATCTCTCCACTGCACTCC 27780

Qy      27754 AGCCTGGGTGACACAGCAAGACTCTATCTCAAAACAACAATAACAACAACAACGAAAAAC 27813
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Qy      27814 ATTTAATGGCTGCACCTTGCCTGTGAAAAATGCATTTCTTGGCCAGATGTGGTGGCTCAA 27873
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Db      27841 ATTTAATGGCTGCACCTTGCCTGTGAAAAATGCATTTCTTGGCCAGATGTGGTGGCTCAA 27900

Qy      27874 ACCTGTAATCCCAACACTTTGGGAAGCTAAGGCCAGGAGTTCGAGACGAGCTGGGATATA 27933
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Qy      27934 TAGGAAGACACAATCTCTACAAAAAAAAATCCACAAAATTAGTCAGGCTTATTGTTCATG 27993
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Db      27961 TAGGAAGACACAATCTCTACAAAAAAAAATCCACAAAATTAGTCAGGCTTATTGTTCATG 28020

Qy      27994 CCTGTAGTCCCAGGTACTCAGGAGGCTGAGGCAGGATTCCTCAAGCCCAGGAGTTCAAGG 28053
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Qy      28054 CTTCCGTGAGCTATGATGGCACAACTGCACTCCATCTTGGGTGACAGAGCAAGGTCCTAT 28113
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Db      28081 CTTCCGTGAGCTATGATGGCACAACTGCACTCCATCTTGGGTGACAGAGCAAGGTCCTAT 28140

Qy      28114 CTCTGGAGAAAAAAAAAAAAAAGAAGGCATTTCTTAGGAGAGTTCTTCTCTGTAGAGTCCT 28173
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Db      28141 CTCTGGAGAAAAAAAAAAAAAAGAAGGCATTTCTTAGGAGAGTTCTTCTCTGTAGAGTCCT 28200

Qy      28174 AAGGGTTCCATGGAACTCCTTAAAAGCATCAGAGTATGTGAGTGCAATGGGAGGAAGCAT 28233
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Db      28201 AAGGGTTCCATGGAACTCCTTAAAAGCATCAGAGTATGTGAGTGCAATGGGAGGAAGCAT 28260

Qy      28234 TTAGCCAGAGCAGTTGTGCTCCCATTGCATATTAATTTTTAAAAAACAAAGCTATAAAAA 28293
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Qy      28294 AAAGTTGAAAACTACTACGTTAGCATCAGCCTGACATTTAATGGCCTCGTAAATCAAACC 28353
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Db      28321 AAAGTTGAAAACTACTACGTTAGCATCAGCCTGACATTTAATGGCCTCGTAAATCAAACC 28380

Qy      28354 TTAATTGACTTTTTAGCCAGTTATGCTACTAGCCAACTACAGACAACACACTTTTTAACC 28413
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Qy      28414 AAATTAGACTAATAGTTGTCATCAGTGGAAATCAAGTTTGCCATTCTTCCATGCCTTTGC 28473
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Qy      28474 TCACACCATTACCTTTTCTGGAATGTCCTGTACTCATCTTCCTGTGTTGAACTCTATACC 28533
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Db      28501 TCACACCATTACCTTTTCTGGAATGTCCTGTACTCATCTTCCTGTGTTGAACTCTATACC 28560

Qy      28534 CAACTTTAAAAACCTAGCTCAAAGTTCAACACTTCCATTCCATTTCAAAAAGAGCTTTCC 28593
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Qy      28594 TCTTCCTTAAAGTTTAAGAACTCATTTTCATGAATCTTTTTGGCATTTATTGCACACATG 28653
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Qy      28654 CTTGCTTTGTGTTATTTGTGTTCAGCCTCATATGCCCCCAAGGTGTTTTAGACTCCTTAA 28713
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Qy      28714 CGGCAAAAATGATGCTCTAAACACCTTTCTATCTTTCATAGTGTCTTAGTCTGTTTGTGT 28773
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Qy      28774 TGCTATAAAGGAATACCTGAGGCTGGGGAATTTATTTAAAAAAGAGGTTTATTTGGCTCA 28833
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Qy      28834 CAGTTCTGCAGCTATATAAGAAGCATAGTGTCAGCATCTGCTTCAGGTGAGGGCTTCAGG 28893
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Qy      28894 AAGTTTCCACCCATGGTAGAAGGCAAAGGGGAGCAGGCATCACATATCAAGAGAGGAGGA 28953
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Qy      28954 AAAAAAGGAAGGAAGAAAGGAGGGTGCCATTCTCTTTCAACAATCAGTTCTTGTGGGAAC 29013
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Qy      29014 TAATGGGACAAGAGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCCCTTTGGGAGAC 29073
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Qy      29074 CAAGGTGGGTGGATCACCTGAAGTCAGAAGCCTGAGACCAGCCTGGCCAATGTGGTGAAA 29133
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Qy      29134 CTCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCCTGGTGGCGTGTACCTGTAGTCCC 29193
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Qy      29194 AGATACTCAGGAGGCTGAGGTAGGATAATCACTTGAACCCGGAAGACAGAGGTTGCAGTG 29253
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Qy      29254 AGCTTGTGCCACTGCACTCCAGCCGGGGCAACAGAGTGAGACGGTCTCAAAAAATTTTAA 29313
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Qy      29314 AAACTTTAAAAATAATAGAGCAAGAAAGCACCAAGTTATTCAGGAGGGATCCACCCCCAA 29373
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Qy      29374 TGACTCAAATACCTCCCACCAGGCCTCACTTCCAACACTGGGGATCAATTTCCGTATGAG 29433
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Qy      29434 ATTTGGAGGAGACAAATATCCAAACTATATCACATAGTAATGAACATAGTACCTTATCTA 29493
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Qy      29494 TAGAAAGCAATGGCTAGACAACTGTTGAATGGCTAACCAAATCTGCTTTCCTATGGTCTC 29553
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Qy      29554 GCTCTAGAGGGGGTCAGTATGAGTTTCTGTCAAAAGGAGAAAAAAAAATGTATAGTCAGT 29613
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Qy      29614 TTTGTGTGTGTGTGTGTTCATGTAAAAGAGATCAAGAGAAAAGAACAAGAGAAATCATGA 29673
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Qy      29674 AAAGGAGGGGGAATATAAGAATAATACATAGAAAAAAGCAAATTATCTTGTTTATCAGTA 29733
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Qy      29734 ATACCCAAGGGGGTAGAAATGGTAAGTAATAATCCTTCTTCACTTTGTCTGTAGTTCACT 29793
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Qy      29794 TTTTTGCACCTTTATTTTGATGAATTCACATCGAAGACATTAACTCATTAAGGCTTCCAA 29853
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Qy      29854 TATTTTTGGAGATAAGAAGGGCTGCTATGCTCTTTATAGATGGAAAACTTGGGTCATTAA 29913
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Qy      29914 TAACTCAAACAAGGACATAACAAAGAAATGGAGCATAAACTGCCAGGTCCTGACTGTAGA 29973
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Qy      29974 TTTGGATTCCCAGTTGGTGTCTTGTCACCCTTTGTTACTCTTCCTAAAGTTATGATCTTT 30033
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Qy      30034 TCTTGTGCATAGGAAATTCATAGTGATTTCCCATCACCCTTGGGATTATCATAGCTCCTT 30093
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Db      30181 GTGTATATCATTGTGTTCTCACGCAGCACCCACAGATCTCACCAAGAACCTAGCTGAAGC 30240

Qy      30214 CTGTAGAATGAATAGGTAAGTACTGCCATGCCAATCTGGAGTACTCAAGCGATGCAAATG 30273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30241 CTGTAGAATGAATAGGTAAGTACTGCCATGCCAATCTGGAGTACTCAAGCGATGCAAATG 30300

Qy      30274 ATTCCTTTAATTGTACTTTTGCAGGCTTGTCAGTTTTGCTCATGGAGAAGTGGCTACTGC 30333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      30301 ATTCCTTTAATTGTACTTTTGCAGGCTTGTCAGTTTTGCTCATGGAGAAGTGGCTACTGC 30360

Qy      30334 ATCCATGTTATATCTATGTAATGTTGGACTGCGAAGCATCACTTGACTTTTTCCAAGCAG 30393
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Db      30361 ATCCATGTTATATCTATGTAATGTTGGACTGCGAAGCATCACTTGACTTTTTCCAAGCAG 30420

Qy      30394 AAATTACAGCTGATGACAAGCTGCTGCTGAGAAAATGGATATTTTTCTGAATTCAGTTCT 30453
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Db      30421 AAATTACAGCTGATGACAAGCTGCTGCTGAGAAAATGGATATTTTTCTGAATTCAGTTCT 30480

Qy      30454 ACGTGGAAACAGCTGACTAGTTTCCATTGCTGTAAGAATGGCTCTTTTGCTCTTGGTTGA 30513
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Db      30481 ACGTGGAAACAGCTGACTAGTTTCCATTGCTGTAAGAATGGCTCTTTTGCTCTTGGTTGA 30540

Qy      30514 TTTTGAGTAATGGCTTTACTTCTGTAGAAAGGAGATTTCATTTGAAGTCCACTCAGGGAT 30573
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Db      30541 TTTTGAGTAATGGCTTTACTTCTGTAGAAAGGAGATTTCATTTGAAGTCCACTCAGGGAT 30600

Qy      30574 TTGGTTCAACAAACTGGAGTACAGGTTTCAGAAAATATCTCTTTAATCCTCCAATAATAA 30633
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Qy      30634 ATTTTCTCATCTATAATTCCTGGAACACTTCATCCTTTGCAGCCGAGCATATAGATAGAT 30693
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Db      30661 ATTTTCTCATCTATAATTCCTGGAACACTTCATCCTTTGCAGCCGAGCATATAGATAGAT 30720

Qy      30694 TTGTTGCTCACTGTGTTCTGATTGCCACTTTGACCTGCTTTTTCAACTTAGGTTACAAAT 30753
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Db      30721 TTGTTGCTCACTGTGTTCTGATTGCCACTTTGACCTGCTTTTTCAACTTAGGTTACAAAT 30780

Qy      30754 AGAACAGAATCTCTCTGATTTTTCTCATTAATTGTTTGAATTCCCACTTTTCCTCATTAG 30813
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Db      30781 AGAACAGAATCTCTCTGATTTTTCTCATTAATTGTTTGAATTCCCACTTTTCCTCATTAG 30840

Qy      30814 CAAGAAGTCCAGTATCTTCCTGAGAACTTCCTTTTCTCAATCTAGGAACTTACTTGGTCC 30873
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Db      30841 CAAGAAGTCCAGTATCTTCCTGAGAACTTCCTTTTCTCAATCTAGGAACTTACTTGGTCC 30900

Qy      30874 ATAAGGTAACAGTCTTATTTCTGACTATCAAGGAGAGAAATAACAGGAGCCATTATCATC 30933
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Db      30901 ATAAGGTAACAGTCTTATTTCTGACTATCAAGGAGAGAAATAACAGGAGCCATTATCATC 30960

Qy      30934 TTCATGGTGTCACTTTTGAAAACTGGTCCTCTGTAGATCTTCAGATTCTTGCGTTAGTCC 30993
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Db      30961 TTCATGGTGTCACTTTTGAAAACTGGTCCTCTGTAGATCTTCAGATTCTTGCGTTAGTCC 31020

Qy      30994 ATTCAGCTGCTATAACAAAATTGCATAGACAGCATGGCTTATAAATAACAGAAATGTATT 31053
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Db      31021 ATTCAGCTGCTATAACAAAATTGCATAGACAGCATGGCTTATAAATAACAGAAATGTATT 31080

Qy      31054 TCTGACAGTTCTGAAGGCTAGAAAGTCAAAGATTAAGACACTGGCTGATTTGGTGTCTGG 31113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31081 TCTGACAGTTCTGAAGGCTAGAAAGTCAAAGATTAAGACACTGGCTGATTTGGTGTCTGG 31140

Qy      31114 CGAAGGCCCATTTGCTCATAGATGGACGATGACCTTTCACTCTGTCTGCACATGGCAGAA 31173
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Db      31141 CGAAGGCCCATTTGCTCATAGATGGACGATGACCTTTCACTCTGTCTGCACATGGCAGAA 31200

Qy      31174 GGGCAAGAGAGCTCTCTGGGTCTTTTTTATAAGGGCACTAATCTCATTTTTGAGGACCCT 31233
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Db      31201 GGGCAAGAGAGCTCTCTGGGTCTTTTTTATAAGGGCACTAATCTCATTTTTGAGGACCCT 31260

Qy      31234 GCCCCCATGACTTAATCACCTCCCAAAGGCACTGTCTCCCAATACCATCACCTTGAGGGT 31293
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Db      31261 GCCCCCATGACTTAATCACCTCCCAAAGGCACTGTCTCCCAATACCATCACCTTGAGGGT 31320

Qy      31294 TAGGATTTCAACATATGATTTTGGGGGGACAGAAACACGCAGTCCATCTCGCTTGTCCAC 31353
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Db      31321 TAGGATTTCAACATATGATTTTGGGGGGACAGAAACACGCAGTCCATCTCGCTTGTCCAC 31380

Qy      31354 TCCATGGTGGTATTCTTGCTGGATCAGTTTCCTCCTTGGGGTGCATTTGTGTTCCATGTC 31413
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Db      31381 TCCATGGTGGTATTCTTGCTGGATCAGTTTCCTCCTTGGGGTGCATTTGTGTTCCATGTC 31440

Qy      31414 TAACTTGCAAGTTATAGCAGGCCCGATAGCAAAGTATTCCAATGTTGGTATGCAGAGGCA 31473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31441 TAACTTGCAAGTTATAGCAGGCCCGATAGCAAAGTATTCCAATGTTGGTATGCAGAGGCA 31500

Qy      31474 TTGAATAATCAGAATGAACCCACGCCATAAACAACTGGTAGAGCTGCAGAGAGTACCAGC 31533
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Db      31501 TTGAATAATCAGAATGAACCCACGCCATAAACAACTGGTAGAGCTGCAGAGAGTACCAGC 31560

Qy      31534 TGATTATGAGCCCTGGGTAACAGTGGTTTTTAGTTCCTATGTCCGTCAGCCCTTTTCTCC 31593
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Db      31561 TGATTATGAGCCCTGGGTAACAGTGGTTTTTAGTTCCTATGTCCGTCAGCCCTTTTCTCC 31620

Qy      31594 CATAGTAGCCCCACTGTGTTGAAGTGGCTGAATCGACAGAAGCTTCCAGCTTGGGCCACA 31653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31621 CATAGTAGCCCCACTGTGTTGAAGTGGCTGAATCGACAGAAGCTTCCAGCTTGGGCCACA 31680

Qy      31654 TGCTCATGGAACCAATTCTCCTTATGAGCCGTACAAGAGCTGGGTTGCCATTCTGGATAC 31713
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Db      31681 TGCTCATGGAACCAATTCTCCTTATGAGCCGTACAAGAGCTGGGTTGCCATTCTGGATAC 31740

Qy      31714 CCTCTTTTTTTCAAGAGATTTTATTTCAAGGATATTTTTTCTTTTATCAACTACAGGGATT 31773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31741 CCTCTTTTTTTCAAGAGATTTTATTTCAAGGATATTTTTTCTTTTATCAACTACAGGGATT 31800

Qy      31774 ATTTAGAATCTTAGGGCAGTGGTGCCCAACCTTTTTGGCCCCAGGGACAGGTTTTGTGGG 31833
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Db      31801 ATTTAGAATCTTAGGGCAGTGGTGCCCAACCTTTTTGGCCCCAGGGACAGGTTTTGTGGG 31860

Qy      31834 AGACAGTTTTTCCATGGACCAGTGTCAGGGGGCTGGGAGGCATGGTTTTGGGATGAGTCA 31893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31861 AGACAGTTTTTCCATGGACCAGTGTCAGGGGGCTGGGAGGCATGGTTTTGGGATGAGTCA 31920

Qy      31894 AGTACATTACGTTTGTTGTATACTTTATTTCTATTATTATTATATTGTAATATATAATGA 31953
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Db      31921 AGTACATTACGTTTGTTGTATACTTTATTTCTATTATTATTATATTGTAATATATAATGA 31980
Qy      31954 AATAATTACACAACTCACCATAATGTAGGAATCAGTGGGGAGCCCTAAGTTTGTTTTCCT 32013
Db      31981 AATAATTACACAACTCACCATAATGTAGGAATCAGTGGGGAGCCCTAAGTTTGTTTTCCT 32040
Qy      32014 GCAACTAGACAGTCCCATCTGGGGGCAATGGGAGATAGTGACAGATCATCAAGCATTAGA 32073
Db      32041 GCAACTAGACAGTCCCATCTGGGGGCAATGGGAGATAGTGACAGATCATCAAGCATTAGA 32100
Qy      32074 TTCTCATAAGGAGTGCTCAGCCTAGATCCCCGGCATGTGCAGTTCACAATAGGATTTGCT 32133
Db      32101 TTCTCATAAGGAGTGCTCAGCCTAGATCCCCGGCATGTGCAGTTCACAATAGGATTTGCT 32160
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Db      32161 CACCTATGAGAATCTAATGCCACTGCTGATCTGACAGGAGGTGGAGCTCGGGCAGTAATG 32220
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Db      32221 CGAGGGTTGGGGAGCAGCTGTCAATATAGATGAAGCTTTGCTCGCTCGCCTGCCACTCAC 32280
Qy      32254 CTCCTGCTGTGTGGTCCACTTCCTAACAGGTCACAGACTGGTACTGGTCCATGGCCAGGG 32313
Db      32281 CTCCTGCTGTGTGGTCCACTTCCTAACAGGTCACAGACTGGTACTGGTCCATGGCCAGGG 32340
Qy      32314 AGTTGGGGACCCTGTCTTAGGGAGTAGGGGTGGAGTTCCCTTCACTTCTAGAAGGCCCTG 32373
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Db      32401 GATTAGTATCCCAGAGCTGTCATTACAGAGTATCACAAACCAGGTGGCTAAAAACAGACA 32460
Qy      32434 TGAATTCTCTCTTATTTTTGATGGCTTGGAAGTCCAAAGTCAAGGTGCTGCCAGGGCCAT 32493
Db      32461 TGAATTCTCTCTTATTTTTGATGGCTTGGAAGTCCAAAGTCAAGGTGCTGCCAGGGCCAT 32520
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Db      32521 GCTCCCTCTGAAATGTGTAGGGGAGAATCCTTCCTTCCTCTTTCTAGCTTCTGGTGGTTT 32580
Qy      32554 GCTGGCAATCACTGGCATCGCTTGGCTTGCAGCACTTCAACATCTGCCTTTACTGTCTCA 32613
Db      32581 GCTGGCAATCACTGGCATCGCTTGGCTTGCAGCACTTCAACATCTGCCTTTACTGTCTCA 32640
Qy      32614 TAGTGTTCTCCCCTCATGTCTCCAGGTCTCTCTGTCTCTCTTCTTTGTATAAGGAAACTA 32673
Db      32641 TAGTGTTCTCCCCTCATGTCTCCAGGTCTCTCTGTCTCTCTTCTTTGTATAAGGAAACTA 32700
Qy      32674 GTCATATTGGATTAAGGGCCAACCCTACTCTAGTATGACCTCATCTTAAGGTCACATGCA 32733
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Qy      32734 ATGACTATTCCAGATAAGGTCACATTCTGAAGAACTGGGAGTTAGGACTTCATATCTTTT 32793
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Db      32821 GAAGGAACACAGTTCAACCAATAACAGCCCCTGTACTGTTTTACAAATAGGTATTCCTCT 32880
Qy      32854 CCTTCCCAAAGTTCTTCATAGCAGAGACAACTTGTACCAAAAGGCAAAATACCTTATTAT 32913
Db      32881 CCTTCCCAAAGTTCTTCATAGCAGAGACAACTTGTACCAAAAGGCAAAATACCTTATTAT 32940
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Db      33421 TAGCAGCAACGTCAGGGATTGAATTCTTAGGGCAGCAGGCTGGGCACAGTGGCTCATGCC 33480
Qy      33454 TGTAATCCCAGTACTTTGGGAGGCTGAGATGGGTGGATCACTTGACATCAGGTGTTCGAG 33513
Db      33481 TGTAATCCCAGTACTTTGGGAGGCTGAGATGGGTGGATCACTTGACATCAGGTGTTCGAG 33540
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Db      33901 CAAGTTTGAGGAACTATGAGACCAGGCAGTGGGGAACACCACTAGCAGAAATGATGGAAG 33960
Qy      33934 TTCTCAAGAATAACAACAGAGAAATAGACCATGGCCAGAGTCTAGAACCCTCCAGGGAAA 33993
Db      33961 TTCTCAAGAATAACAACAGAGAAATAGACCATGGCCAGAGTCTAGAACCCTCCAGGGAAA 34020
Qy      33994 GGAGATGGGCTCCAGAGGCAGAAGAGGACGTTGAAGGGAATGGGGAGTGGGTGAAATATA 34053
Db      34021 GGAGATGGGCTCCAGAGGCAGAAGAGGACGTTGAAGGGAATGGGGAGTGGGTGAAATATA 34080
Qy      34054 TAGACGATGGGGACCACCCAAGAGCAGTCGCTATTGCAAAACTGAGGAGAAGGAGAGTCT 34113
Db      34081 TAGACGATGGGGACCACCCAAGAGCAGTCGCTATTGCAAAACTGAGGAGAAGGAGAGTCT 34140
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Qy      34114 GGAGGGGGTGGTGGGAAGCTGGGTCTCCTAAGGAGGTTTTGACAAAAGCAGTCATGGAGC 34173
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Db      34141 GGAGGGGGTGGTGGGAAGCTGGGTCTCCTAAGGAGGTTTTGACAAAAGCAGTCATGGAGC 34200

Qy      34174 GGGCTTAGAAATCACAGTTGGGGACAGGGTAAAGTTCCTCGGGATATAGAGGATGAGATT 34233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      34234 AGAAGAGGTTCCAACTAGGGTAGTGTGGAGAAAAGCACTATTGACCCAAAAAGGAAGGAG 34293
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Qy      34294 AATGTGGGTGGAAGTGGCAGAGAAAGAGGGGTTTGAGCAGAGAGTGGTGATTTTTCTAAT 34353
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Db      34321 AATGTGGGTGGAAGTGGCAGAGAAAGAGGGGTTTGAGCAGAGAGTGGTGATTTTTCTAAT 34380

Qy      34354 GCAGAGTTGTGGGAGGTGGAGTGCAGGGAGCCAGGCTGGGTGGCTGTGCTGATGTGATTA 34413
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Db      34381 GCAGAGTTGTGGGAGGTGGAGTGCAGGGAGCCAGGCTGGGTGGCTGTGCTGATGTGATTA 34440

Qy      34414 AGCACTTACTGACTGCCAGGCAATGGGCTAAGTACCTGAGATGCTTTGTCTGTTATCCCT 34473
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Db      34441 AGCACTTACTGACTGCCAGGCAATGGGCTAAGTACCTGAGATGCTTTGTCTGTTATCCCT 34500

Qy      34474 CCCGAAACCCCTCTGAGCAGGTGCAGTTATTATTCTCACTTCACAGATAAGGAAATTGAG 34533
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Qy      34534 GCACAGAGAATTGAGTAACTTACCCAAGGTGACATAGCTCATATATGGTAAAGCAGGCTT 34593
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Db      34561 GCACAGAGAATTGAGTAACTTACCCAAGGTGACATAGCTCATATATGGTAAAGCAGGCTT 34620

Qy      34594 TGAACTCAGTCTAGCTCCCGAACCTAAGCTTGTAACTACTATGCTTTTCCCAAAAAAAGG 34653
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Db      34621 TGAACTCAGTCTAGCTCCCGAACCTAAGCTTGTAACTACTATGCTTTTCCCAAAAAAAGG 34680

Qy      34654 GGGCTGGCACAAAAAGAGCTGAGGGGGCTGGGCATGGTGGCTCATGCCTGTAATCCCAGC 34713
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Db      34681 GGGCTGGCACAAAAAGAGCTGAGGGGGCTGGGCATGGTGGCTCATGCCTGTAATCCCAGC 34740

Qy      34714 ACTTCGGGAGACTGAGGCAGGTGGTTCACCAGAGTTCAGGAGTTCGAGACCAGCCTGGTC 34773
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Db      34741 ACTTCGGGAGACTGAGGCAGGTGGTTCACCAGAGTTCAGGAGTTCGAGACCAGCCTGGTC 34800

Qy      34774 AACATGGTGAAGCCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGTGGTGTGC 34833
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Qy      34834 ACCTGTAGTCCCAGCTACTTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCCAGAGGC 34893
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Db      34861 ACCTGTAGTCCCAGCTACTTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCCAGAGGC 34920

Qy      34894 GGATGTTGTAGTGAGCCAAGATCATGCCACTGGACTCCAGCCTGGGTGACAGAGTGAGAC 34953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      34921 GGATGTTGTAGTGAGCCAAGATCATGCCACTGGACTCCAGCCTGGGTGACAGAGTGAGAC 34980

Qy      34954 TCCATCCAAAAAAAAAGAAGAGCTGAGGTGATGGCCACCATCAGCATCAGCCTGGAAGTTA 35013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      35014 TAGCAGGATGCTAAGTTTCTCTAAAGCTGTCTTTCTTAGGACTTGAAAAAGATAACTTGG 35073
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Qy      35074 GTTTGTATCCCATCTCTGCCATTAGTAGTTTACTGGCTTTGGATAAATTACTTAGCCTTA 35133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35101 GTTTGTATCCCATCTCTGCCATTAGTAGTTTACTGGCTTTGGATAAATTACTTAGCCTTA 35160

Qy      35134 CTGAACCAACTTTGGATTTTTATAGAGATACTGTAATGAAAGGAATAAGGTATCAGTCTT 35193
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Db      35161 CTGAACCAACTTTGGATTTTTATAGAGATACTGTAATGAAAGGAATAAGGTATCAGTCTT 35220

Qy      35194 AGCAGAGCATCCAGAGTGTTCCTATTAAAACCTAAATCATATCCTGTCATTGCTGTGCCC 35253
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Db      35221 AGCAGAGCATCCAGAGTGTTCCTATTAAAACCTAAATCATATCCTGTCATTGCTGTGCCC 35280

Qy      35254 CAAACCATTCAATGGCTTCCCAACTCAAAGTTAAAAACTCATCTTTCCAGTGGCCTGCAA 35313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35281 CAAACCATTCAATGGCTTCCCAACTCAAAGTTAAAAACTCATCTTTCCAGTGGCCTGCAA 35340

Qy      35314 GAGCCTATGCTATCCGGTGTCTGACCTCATCTGTTGTTCCTTTCTCCCTCCCTTTCTTGG 35373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35341 GAGCCTATGCTATCCGGTGTCTGACCTCATCTGTTGTTCCTTTCTCCCTCCCTTTCTTGG 35400

Qy      35374 CTCCAGACGCACTCTGGTCTCCTTGCTGTTCCTTGAATACACCAGGCACACTCTCTTCGC 35433
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Db      35401 CTCCAGACGCACTCTGGTCTCCTTGCTGTTCCTTGAATACACCAGGCACACTCTCTTCGC 35460

Qy      35434 CTGAAACACTTTACCCCAGATATCTTAGCTTACTCTCTGCCTCCCTCAATTCATTGATGA 35493
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Db      35461 CTGAAACACTTTACCCCAGATATCTTAGCTTACTCTCTGCCTCCCTCAATTCATTGATGA 35520

Qy      35494 AATGTCTCAGTGAAGTCTTCTCTCTCTCCTCTGTAAAAGTATACTCTCTGTTCCCCTTCT 35553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35521 AATGTCTCAGTGAAGTCTTCTCTCTCTCCTCTGTAAAAGTATACTCTCTGTTCCCCTTCT 35580

Qy      35554 TTACTGTTCTAGCTACTATTGCTGTGTAACAAATCACTCCCCAAATTTAATGAGTGAAAA 35613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35581 TTACTGTTCTAGCTACTATTGCTGTGTAACAAATCACTCCCCAAATTTAATGAGTGAAAA 35640

Qy      35614 CATCAGCCATCATCTTATTTCTCACGGTTTCTGAGGGTCAGGAATTCTGGAAGGGCTCAG 35673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35641 CATCAGCCATCATCTTATTTCTCACGGTTTCTGAGGGTCAGGAATTCTGGAAGGGCTCAG 35700

Qy      35674 CTGGGAGGTTCTGGCTCTATAATCTCTTATGCAGTGAGAGTCAGATGCTGGCTAAAACTG 35733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35701 CTGGGAGGTTCTGGCTCTATAATCTCTTATGCAGTGAGAGTCAGATGCTGGCTAAAACTG 35760

Qy      35734 AAACAAAGCAGGGTTCTAGTAGCTGAGGGCTGGCTGGGTCTCTCAGATATAGTTCAGATC 35793
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35761 AAACAAAGCAGGGTTCTAGTAGCTGAGGGCTGGCTGGGTCTCTCAGATATAGTTCAGATC 35820

Qy      35794 TCCTCCAGGGGGTCTCTCCACGTGGGCTAGTCTGAACTTCCTCACAGCATGGTGGCCTCA 35853
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35821 TCCTCCAGGGGGTCTCTCCACGTGGGCTAGTCTGAACTTCCTCACAGCATGGTGGCCTCA 35880

Qy      35854 GGGCAGTGGACTCTGCATAGTGGCTGAAGGCTTCGCAGCTGAGTATTCCAGCAAGCAAAG 35913
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35881 GGGCAGTGGACTCTGCATAGTGGCTGAAGGCTTCGCAGCTGAGTATTCCAGCAAGCAAAG 35940

Qy      35914 TGGGAGCTGTATTGCCTCATATGACCCAACCTTGGAATCCACACAGCATCACTTCCGTGT 35973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      35941 TGGGAGCTGTATTGCCTCATATGACCCAACCTTGGAATCCACACAGCATCACTTCCGTGT 36000

Qy      35974 ATTCTACGGGTTGAAAAGTCACAAAAACCAACCAGTTTCAAGGAGAAGGAACAGAGATCA 36033
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Db      36001 ATTCTACGGGTTGAAAAGTCACAAAAACCAACCAGTTTCAAGGAGAAGGAACAGAGATCA 36060

Qy      36034 CATTTCTCAATTGGAGAAGGGTCAAAGTCACATTGTAATCAGAGCCTATGGGATACGAAG 36093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36061 CATTTCTCAATTGGAGAAGGGTCAAAGTCACATTGTAATCAGAGCCTATGGGATACGAAG 36120

Qy      36094 TATTGCGGTCAGGTATGAAAAATTTGATTTGCTGCATCTGCTTTACTTTCTCCACAGCGT 36153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36121 TATTGCGGTCAGGTATGAAAAATTTGATTTGCTGCATCTGCTTTACTTTCTCCACAGCGT 36180

Qy      36154 TCATGATCTGCTTCTCACATGATATTGACTTACGTCATTTCTGCGTTTCCTGTCTTCCAC 36213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36181 TCATGATCTGCTTCTCACATGATATTGACTTACGTCATTTCTGCGTTTCCTGTCTTCCAC 36240

Qy      36214 ACTAAAATGTCAGCCTGTTTTGTTCACTGCTGTATCCCCAGAGCCTAGCACGGAGCCCAG 36273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36241 ACTAAAATGTCAGCCTGTTTTGTTCACTGCTGTATCCCCAGAGCCTAGCACGGAGCCCAG 36300

Qy      36274 CATGTAGTGGTATCCAATAAATACTTGTTGCATGAATGAATTCTGTCTTTTAATCCTAGC 36333
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Db      36301 CATGTAGTGGTATCCAATAAATACTTGTTGCATGAATGAATTCTGTCTTTTAATCCTAGC 36360
Qy      36334 TATAGGTTTCTAAGTTAAATATTACTATAATCATCTTACAGACGAGGGAAATGAGGCTCA 36393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36361 TATAGGTTTCTAAGTTAAATATTACTATAATCATCTTACAGACGAGGGAAATGAGGCTCA 36420
Qy      36394 AGAAGATTTGGTAACTTATGCGGGATCACTCAGCCACATAATGGAAGAGACAGCATTGAA 36453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36421 AGAAGATTTGGTAACTTATGCGGGATCACTCAGCCACATAATGGAAGAGACAGCATTGAA 36480
Qy      36454 GTACACATGCTTGCTCTGTCTGCTCTTCCAAGCTGCTCATCACACAGCTGCACCTCTGAG 36513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36481 GTACACATGCTTGCTCTGTCTGCTCTTCCAAGCTGCTCATCACACAGCTGCACCTCTGAG 36540
Qy      36514 GACTTCCCTCCCCAGTCCACCTCCACCCTTACCCAGAGACACACATGGCCACAATCCACT 36573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36541 GACTTCCCTCCCCAGTCCACCTCCACCCTTACCCAGAGACACACATGGCCACAATCCACT 36600
Qy      36574 AGCAGACCAAAATTCAATTTTTCCCCAGTTGGTTGCACTCAAGCTGAGAGCAAAGCAATT 36633
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Db      36601 AGCAGACCAAAATTCAATTTTTCCCCAGTTGGTTGCACTCAAGCTGAGAGCAAAGCAATT 36660
Qy      36634 GCACTTTAAATCCCCTTACAGCAGATATTTCAGAGCATGTTCGGAAGAACCCATCACACT 36693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36661 GCACTTTAAATCCCCTTACAGCAGATATTTCAGAGCATGTTCGGAAGAACCCATCACACT 36720
Qy      36694 TGGCTTTTAGATCTTATTTCTGGTTTGTTACAAAAACACAATTAAATGAAAGGTTAGGTA 36753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36721 TGGCTTTTAGATCTTATTTCTGGTTTGTTACAAAAACACAATTAAATGAAAGGTTAGGTA 36780
Qy      36754 GCTTTTGAATGGCCAGCTCAAAGTTTTGGCTTATTTTTGCCTTGCTGTCTTTATAGGCAT 36813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      36781 GCTTTTGAATGGCCAGCTCAAAGTTTTGGCTTATTTTTGCCTTGCTGTCTTTATAGGCAT 36840
Qy      36814 TTTACCAATATTTATCACTATTTCCCTTAGGGAACCCTTAGATCTGTGATATTTGAAATA 36873
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Db      36841 TTTACCAATATTTATCACTATTTCCCTTAGGGAACCCTTAGATCTGTGATATTTGAAATA 36900
Qy      36874 ATAAAGCCTCTCCATTGGCCCTTTAAAAGGTTTGTGGTAAAACCACACCATTAACATTCA 36933
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Db      36901 ATAAAGCCTCTCCATTGGCCCTTTAAAAGGTTTGTGGTAAAACCACACCATTAACATTCA 36960
Qy      36934 CAGTTCCTTATTTATGAGGCCTGATTGCACTTATTTCCATATTTCTCACTGTTTCTCCGA 36993
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Db      36961 CAGTTCCTTATTTATGAGGCCTGATTGCACTTATTTCCATATTTCTCACTGTTTCTCCGA 37020
Qy      36994 TGAGGATTTCACATAATAGTGTTTGAAGGCTAAAGACTTCAAAGCAGATTCTTTACTATT 37053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37021 TGAGGATTTCACATAATAGTGTTTGAAGGCTAAAGACTTCAAAGCAGATTCTTTACTATT 37080
Qy      37054 TTTATCTTGAAAAATATTCAATATTTGTGTAATTAAAGTGAAGTCTTCCTAGAGAAAATG 37113
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Db      37081 TTTATCTTGAAAAATATTCAATATTTGTGTAATTAAAGTGAAGTCTTCCTAGAGAAAATG 37140
Qy      37114 ACAACTCAAATAATCTTAAATGTACCTCCAAGAAAAAAGCTGTCAAAGTGACATTTAGTA 37173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37141 ACAACTCAAATAATCTTAAATGTACCTCCAAGAAAAAAGCTGTCAAAGTGACATTTAGTA 37200
Qy      37174 ATAGAGTCACATTCTCTAAGGCCTTTGCTTCTCCTTCTGATTCTTATCATCTTTGAAGGT 37233
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Db      37201 ATAGAGTCACATTCTCTAAGGCCTTTGCTTCTCCTTCTGATTCTTATCATCTTTGAAGGT 37260
Qy      37234 TATGTCATGGGCTGACTTCAAATCAACTTTTAAAATTATTATGGCCTTCTTTAAATGTGA 37293
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Db      37261 TATGTCATGGGCTGACTTCAAATCAACTTTTAAAATTATTATGGCCTTCTTTAAATGTGA 37320
Qy      37294 GTTCTGAAGGTGAGGGGCTTTATCTTTCTTTTGCTCCAGATTTTTTTTACCGCGTCATTA 37353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37321 GTTCTGAAGGTGAGGGGCTTTATCTTTCTTTTGCTCCAGATTTTTTTTACCGCGTCATTA 37380
Qy      37354 CCAAGCATCTTAAAACAAAACCTAAAAACAAAAATCTTCCTTGACCTGGTTTTTCCCACT 37413
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Db      37381 CCAAGCATCTTAAAACAAAACCTAAAAACAAAAATCTTCCTTGACCTGGTTTTTCCCACT 37440

Qy      37414 AGCTAACATCCTATTTTTATCTTTCCCCTTTGCACTAAAGGTTTTTAAACGGATCTTTAT 37473
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Db      37441 AGCTAACATCCTATTTTTATCTTTCCCCTTTGCACTAAAGGTTTTTAAACGGATCTTTAT 37500
Qy      37474 ACCCTCTGTCTCCATTTTCTCATCTGCTAACTTATATGGCAAAGATTACCACTGCCTTTC 37533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37501 ACCCTCTGTCTCCATTTTCTCATCTGCTAACTTATATGGCAAAGATTACCACTGCCTTTC 37560
Qy      37534 AACATAATTGGCCAATCTACAGAAAGTTTTCAAGTTCTCTTTTTAATTGACCACCTCCTG 37593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37561 AACATAATTGGCCAATCTACAGAAAGTTTTCAAGTTCTCTTTTTAATTGACCACCTCCTG 37620
Qy      37594 CCTACCTCCCCACCTTTGACATCTTGCTTCTCACTTGGCACCTTACCCAGTGTTCAAGAT 37653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37621 CCTACCTCCCCACCTTTGACATCTTGCTTCTCACTTGGCACCTTACCCAGTGTTCAAGAT 37680
Qy      37654 TCCCTCCTTTAGGATGTCTTCAGAGCAGCTACACAGTTGGTACTATAATTTATACATCCT 37713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37681 TCCCTCCTTTAGGATGTCTTCAGAGCAGCTACACAGTTGGTACTATAATTTATACATCCT 37740
Qy      37714 TGTACACAGGGCTTGCTGGGATATTGATGGAGAGAAGGAGGAAACTGGAAGTAGTTCAGG 37773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37741 TGTACACAGGGCTTGCTGGGATATTGATGGAGAGAAGGAGGAAACTGGAAGTAGTTCAGG 37800
Qy      37774 CCAGAGCTAGGGAAATTGACCCATCTCCAGGTCTCAGGTCTGCAAGGGGAGCTCACAGCT 37833
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Db      37801 CCAGAGCTAGGGAAATTGACCCATCTCCAGGTCTCAGGTCTGCAAGGGGAGCTCACAGCT 37860
Qy      37834 TAACACATGGAGTCTAGAAACTTGTGCTGGACCTTGACCAACACCAGCCCATGGAGTCCA 37893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      37861 TAACACATGGAGTCTAGAAACTTGTGCTGGACCTTGACCAACACCAGCCCATGGAGTCCA 37920
Qy      37894 ATACAGTGCTCAATAGGGATTTCCAGGAAATTGCTATATTTATTCAAAGAGAACTTACCA 37953
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Db      37921 ATACAGTGCTCAATAGGGATTTCCAGGAAATTGCTATATTTATTCAAAGAGAACTTACCA 37980
Qy      37954 AGTGTCAGCTACGTGTTGGGCATTGTGCTAGGCACAGGGACCACAAAGATAAGACATTGT 38013
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Db      37981 AGTGTCAGCTACGTGTTGGGCATTGTGCTAGGCACAGGGACCACAAAGATAAGACATTGT 38040
Qy      38014 AGCTTTCCTTAAGTTGCTCACTGAGTAAATAGAGAGACAGAAAGGTAAACAGGTAAGTGC 38073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38041 AGCTTTCCTTAAGTTGCTCACTGAGTAAATAGAGAGACAGAAAGGTAAACAGGTAAGTGC 38100
Qy      38074 AAAAATACATACAATTCAGCAATAGTGTTCATAGTGGCTATGGAGAGAACGCTCACTAAC 38133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38101 AAAAATACATACAATTCAGCAATAGTGTTCATAGTGGCTATGGAGAGAACGCTCACTAAC 38160
Qy      38134 TTTGTTTAAACAGTTGTTCTTTCAAGGATTTGACATGGATTTGATTGGAAAAGCATGATA 38193
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Db      38161 TTTGTTTAAACAGTTGTTCTTTCAAGGATTTGACATGGATTTGATTGGAAAAGCATGATA 38220
Qy      38194 CCATTTTTTGCAATTAAACACAGGAATACATAAATAAAATGCATCAGTATTTTTTACAAA 38253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38221 CCATTTTTTGCAATTAAACACAGGAATACATAAATAAAATGCATCAGTATTTTTTACAAA 38280
Qy      38254 TAGCTACTAAGAGCTACTAGAAAACCTGGGAATTCTTAAAACCTTACCATGCTACTTGCT 38313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38281 TAGCTACTAAGAGCTACTAGAAAACCTGGGAATTCTTAAAACCTTACCATGCTACTTGCT 38340
Qy      38314 CTAAAATATTTTATTTTATGTTATTTTGTACATTTCTTTACCTACACAAACACCACTGTT 38373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38341 CTAAAATATTTTATTTTATGTTATTTTGTACATTTCTTTACCTACACAAACACCACTGTT 38400
Qy      38374 TTCTTCATTTCTTAGTCTATTTAAACCTCACACCCTTTCAGCATCTCTTAATTATTTACT 38433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38401 TTCTTCATTTCTTAGTCTATTTAAACCTCACACCCTTTCAGCATCTCTTAATTATTTACT 38460
Qy      38434 ACCATCTGTTAGTTCTCCTGTCCTGAATGAAACAAAAATGGCAGAATGTAAAACGAGGGC 38493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38461 ACCATCTGTTAGTTCTCCTGTCCTGAATGAAACAAAAATGGCAGAATGTAAAACGAGGGC 38520
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Qy      38494 GAACAGATTTTTGACAGGAAGTATTCAGAGGTAGAAGGAAATAGTCAAGACACATATGAT 38553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38521 GAACAGATTTTTGACAGGAAGTATTCAGAGGTAGAAGGAAATAGTCAAGACACATATGAT 38580

Qy      38554 AAACGAAAACAATAATAACTTTATACATAACAACTTATAGACACATTTAAAAAGTTTAAG 38613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38581 AAACGAAAACAATAATAACTTTATACATAACAACTTATAGACACATTTAAAAAGTTTAAG 38640

Qy      38614 ATCTCAAGAGCTATGTCTGAATAGATAGGAGTAAAAACTCTATTAAGTAATTAGGAAAAT 38673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38641 ATCTCAAGAGCTATGTCTGAATAGATAGGAGTAAAAACTCTATTAAGTAATTAGGAAAAT 38700

Qy      38674 AACAAGAACAGTGAATTTCTTAATGAATGGCATGTAATCAAAACTGTACTTATCGTCTAA 38733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38701 AACAAGAACAGTGAATTTCTTAATGAATGGCATGTAATCAAAACTGTACTTATCGTCTAA 38760

Qy      38734 TTCATAATCTTGAATGTTTTTATTTTATTTATTTATTTTTTTATTTTTTGAGACAGAGTC 38793
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Db      38761 TTCATAATCTTGAATGTTTTTATTTTATTTATTTATTTTTTTATTTTTTGAGACAGAGTC 38820

Qy      38794 TTGCTCTGTCACCCAGGCTAGAGTACAGTGGCGTGATCTCAGCTCACTGCAACCTCCACC 38853
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Db      38821 TTGCTCTGTCACCCAGGCTAGAGTACAGTGGCGTGATCTCAGCTCACTGCAACCTCCACC 38880

Qy      38854 TCCCAGGTTCAAGCGATTCTGCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGAGGCCT 38913
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Db      38881 TCCCAGGTTCAAGCGATTCTGCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGAGGCCT 38940

Qy      38914 GCCACTGCACCCGGCTAATTTCTGTATTTTTAGTAGAGATGGGGTTTCACCATCTTGGCC 38973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38941 GCCACTGCACCCGGCTAATTTCTGTATTTTTAGTAGAGATGGGGTTTCACCATCTTGGCC 39000

Qy      38974 AGGCTGGTCTTGAACTCCTGACCTCATGATCCACCAGCCTTGGCCTCCCAAAGTGCTGGG 39033
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39001 AGGCTGGTCTTGAACTCCTGACCTCATGATCCACCAGCCTTGGCCTCCCAAAGTGCTGGG 39060

Qy      39034 ATTACAGGCGTGAGCCACCACGCCTGGTCGAATGTCTTTATTATTTGAAGAGACAACATG 39093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39061 ATTACAGGCGTGAGCCACCACGCCTGGTCGAATGTCTTTATTATTTGAAGAGACAACATG 39120

Qy      39094 GGCCTTAAATCTGTCTTCTATTTGACAGACTTTGATGGAGTCAAATCCCAATGCTGCCAC 39153
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Db      39121 GGCCTTAAATCTGTCTTCTATTTGACAGACTTTGATGGAGTCAAATCCCAATGCTGCCAC 39180

Qy      39154 TTACTGAACGGCCTTAAATGACTTAGTCTCTCTCAGCTGTCTTTCTGCATATGTAAGGTG 39213
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Db      39181 TTACTGAACGGCCTTAAATGACTTAGTCTCTCTCAGCTGTCTTTCTGCATATGTAAGGTG 39240

Qy      39214 GAATAATGATGGCTTTCAAGGAGGAATAAACCTATGAAAAGTGTTGAGGATAGTGTTTGA 39273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39241 GAATAATGATGGCTTTCAAGGAGGAATAAACCTATGAAAAGTGTTGAGGATAGTGTTTGA 39300

Qy      39274 TATGAAATAAGGATTTCAACAAGTAGTAGCTGCTATTGAAGATTTAAGAGTTATTTATTA 39333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39301 TATGAAATAAGGATTTCAACAAGTAGTAGCTGCTATTGAAGATTTAAGAGTTATTTATTA 39360

Qy      39334 CAACTATTTAATAAAATTTTAAAAACTAATACACTTAAATTATTAAAGAGCTTTGAAATG 39393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39361 CAACTATTTAATAAAATTTTAAAAACTAATACACTTAAATTATTAAAGAGCTTTGAAATG 39420

Qy      39394 GGCCAGGCGCAGTAGCTCCTGCCTGTAATCCCAACACTTTGGGAGGCCAAGGTGGGCGGA 39453
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Db      39421 GGCCAGGCGCAGTAGCTCCTGCCTGTAATCCCAACACTTTGGGAGGCCAAGGTGGGCGGA 39480

Qy      39454 TCACCTGAGGTCAGGAGTTTAAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACT 39513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39481 TCACCTGAGGTCAGGAGTTTAAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACT 39540

Qy      39514 AAAAACGCAAAAATTAGCCAGGTGTGGTGGCATGCACCTGTAGTCCCAACTACTCAGGAG 39573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39541 AAAAACGCAAAAATTAGCCAGGTGTGGTGGCATGCACCTGTAGTCCCAACTACTCAGGAG 39600

Qy      39574 GTTGAGGGAGGAGAATTGCTTGAACCTAGGAGGTGGAGGTTGCAGTAACCCGAGATGTCA 39633
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Db      39601 GTTGAGGGAGGAGAATTGCTTGAACCTAGGAGGTGGAGGTTGCAGTAACCCGAGATGTCA 39660

Qy      39634 CTGCACTCCAGCCTGGCAACAGAGCAAGACTCCATAAAGACAACAAAAGCTTTGAAATTG 39693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39661 CTGCACTCCAGCCTGGCAACAGAGCAAGACTCCATAAAGACAACAAAAGCTTTGAAATTG 39720

Qy      39694 TGTAAATGAGTTGTACCTATCTTCATTTAAGAAATTCATCTTTGTTCATTTATTTTTACT 39753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39721 TGTAAATGAGTTGTACCTATCTTCATTTAAGAAATTCATCTTTGTTCATTTATTTTTACT 39780

Qy      39754 TGACATGAGAGCTTCCAGCAATTTTTAATTAAGCCCTCACAGATTTTATGTCACTGGCTA 39813
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Db      39781 TGACATGAGAGCTTCCAGCAATTTTTAATTAAGCCCTCACAGATTTTATGTCACTGGCTA 39840

Qy      39814 TGTGATAAACAAATTATTTGCTAAAATAATATTCTTGCTTCTTTTTTTAAGGAATTGTCTC 39873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39841 TGTGATAAACAAATTATTTGCTAAAATAATATTCTTGCTTCTTTTTTAAGGAATTGTCTC 39900

Qy      39874 CCTAGAAACGGTTTGTACCAAACAATACACTGACTTTACACAAAATCAGATCTGATTGGC 39933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39901 CCTAGAAACGGTTTGTACCAAACAATACACTGACTTTACACAAAATCAGATCTGATTGGC 39960

Qy      39934 AACAGTTGCAGATGTTTTCAAAAGATTTTCATTTGAGAAGGGGCCCATTTGGGTTATTTA 39993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39961 AACAGTTGCAGATGTTTTCAAAAGATTTTCATTTGAGAAGGGGCCCATTTGGGTTATTTA 40020

Qy      39994 GATTCTA 40000
              |||||||
Db      40021 GATTCTA 40027
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RESULT 3
AL355340

LOCUS	AL355340 112442 bp DNA linear PRI 13-JUN-2002
DEFINITION	Human DNA sequence from clone RP11-383C6 on chromosome 10, complete sequence.
ACCESSION	AL355340
VERSION	AL355340.17 GI:21436504
KEYWORDS	HTG.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 112442)
AUTHORS	Leongamornlert,D.
TITLE	Direct Submission
JOURNAL	Submitted (13-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT	On Jun 17, 2002 this sequence version replaced gi:16416169. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10

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          RP11-383C6 is from the library RPCI-11.2 constructed by the group
          of Pieter de Jong. For further details see
          http://www.chori.org/bacpac/home.htm
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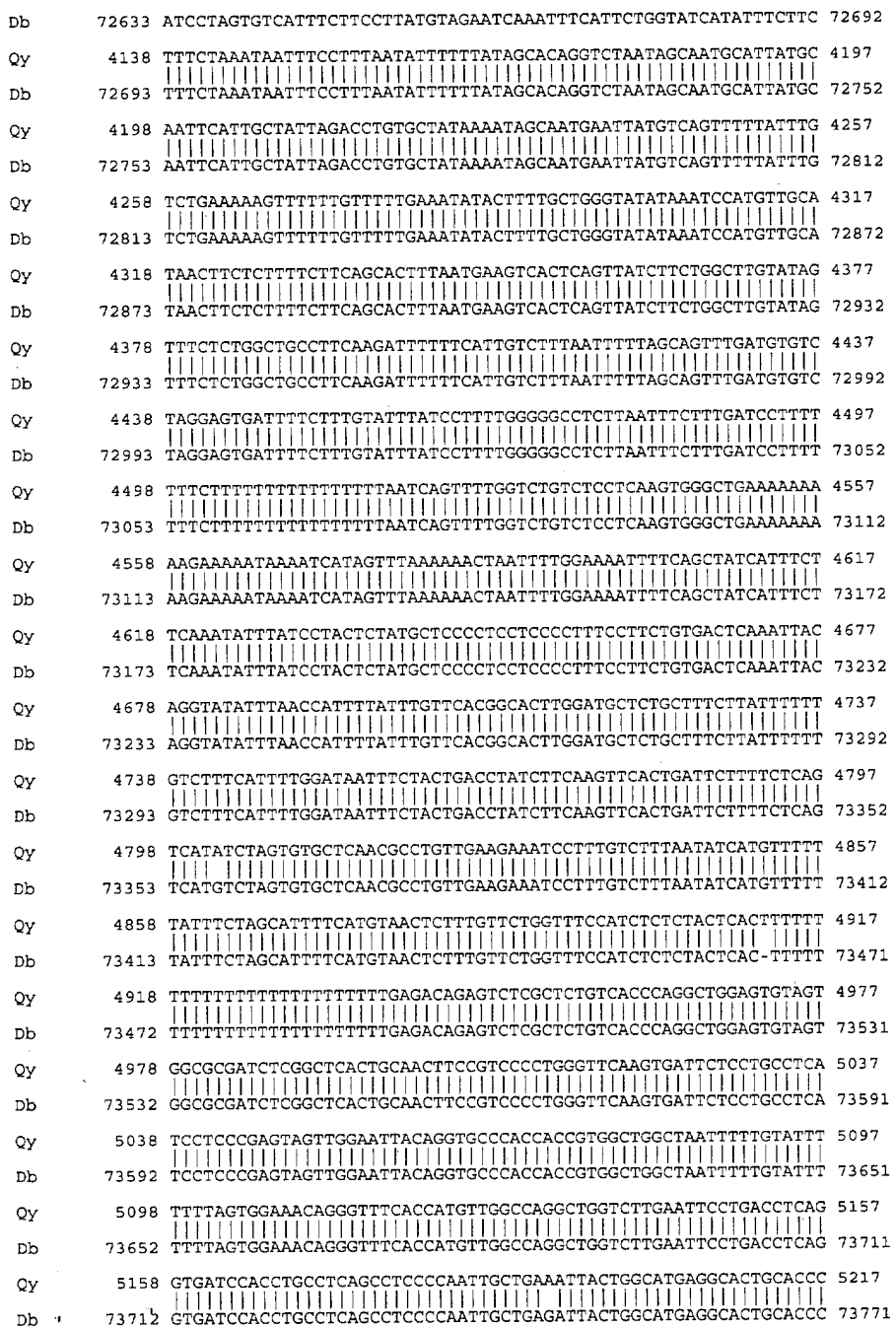
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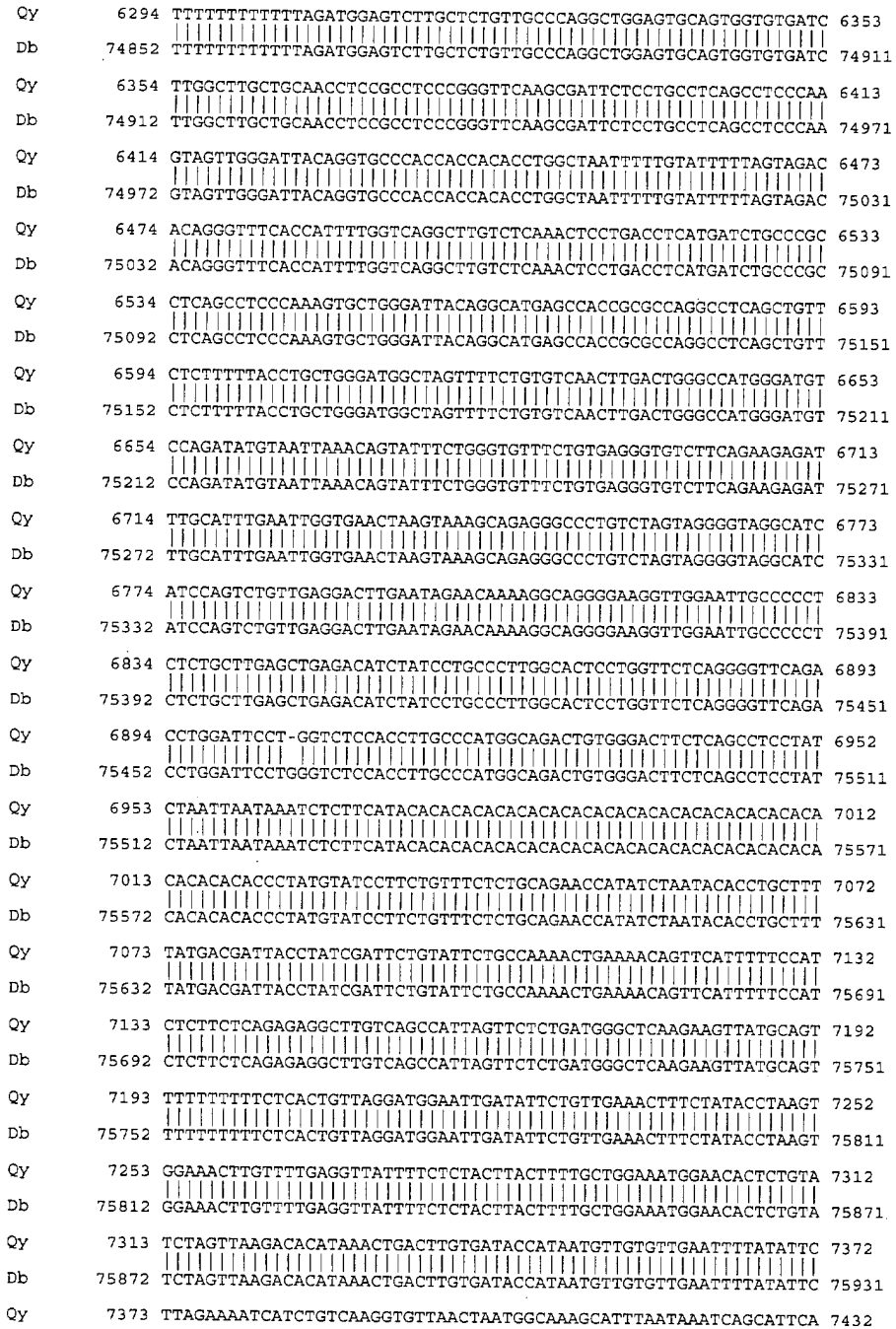
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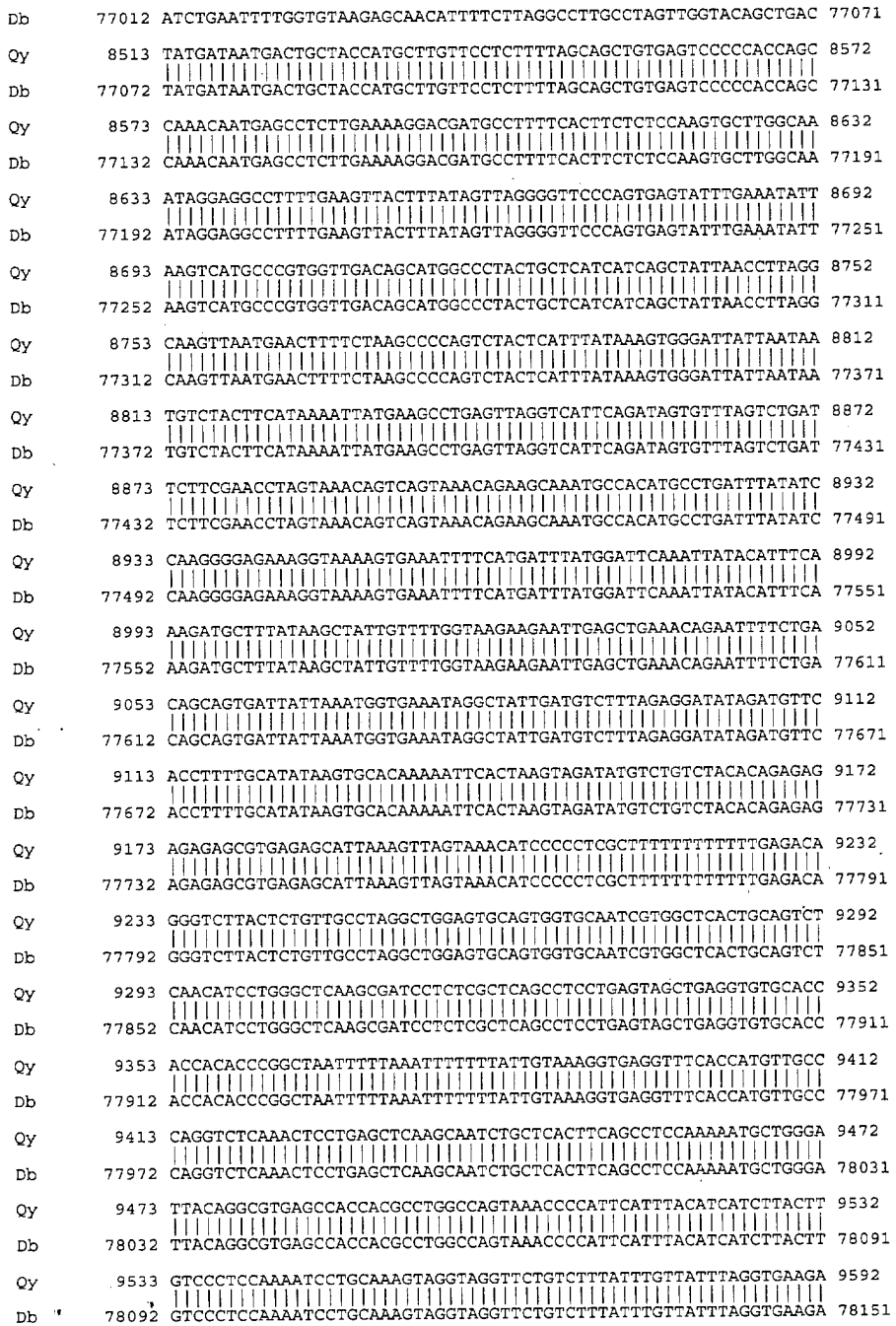
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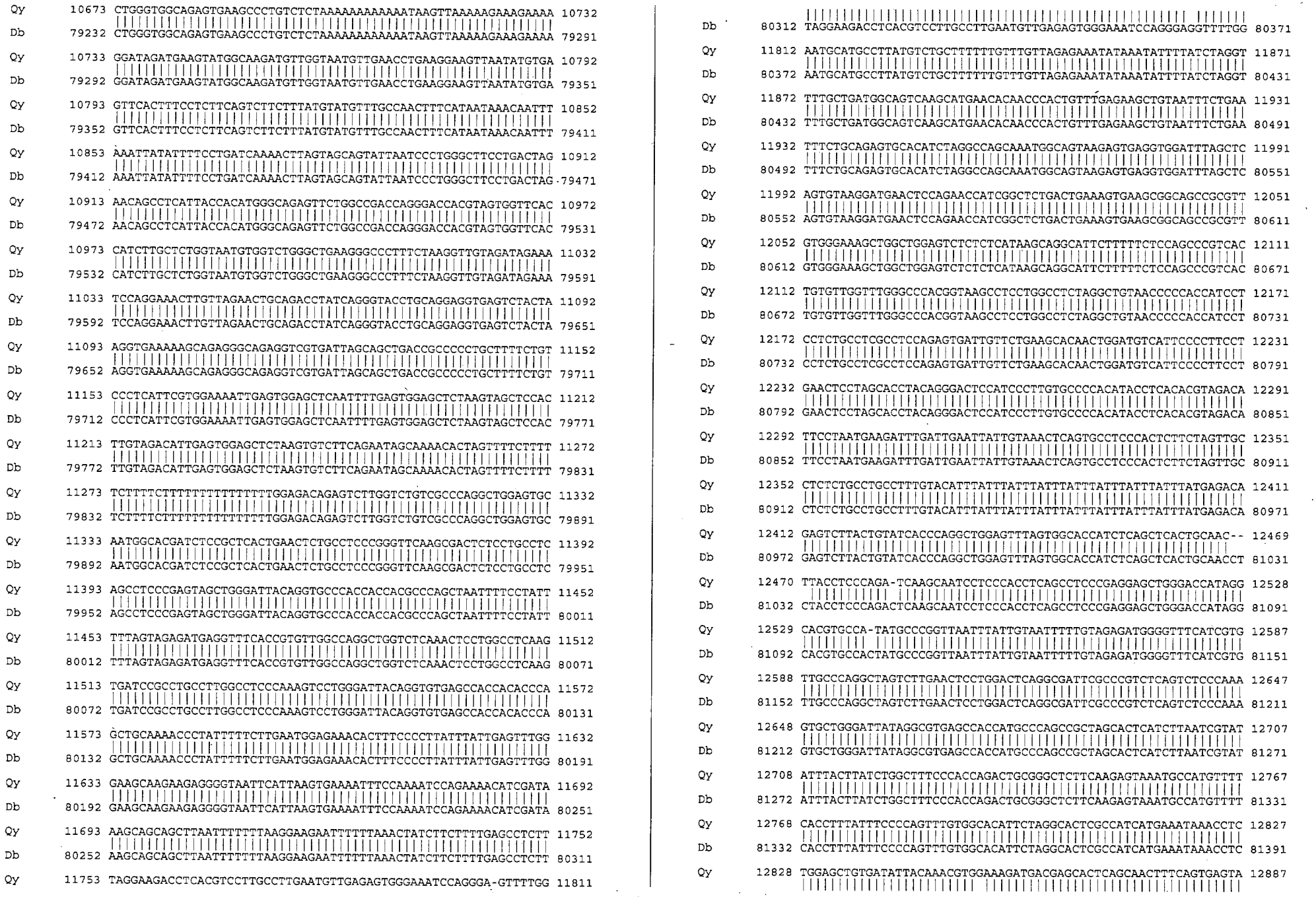
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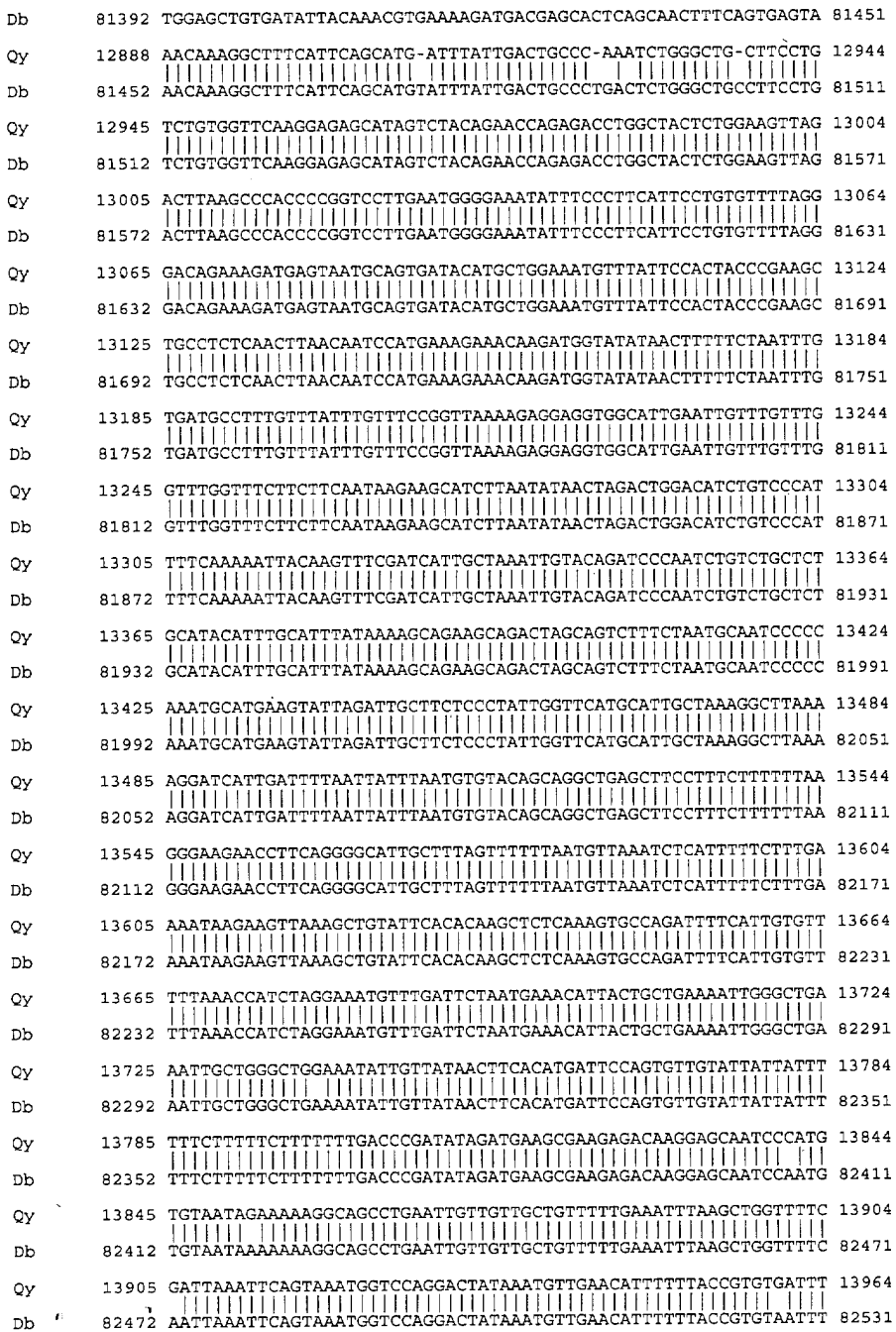
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Db 79112 TGGGCACTGTGGCTCATGCCTATAATCCCAGCATTTAGGAGGCCAAGTTGGGAGGATCAC 79171
Qy 10613 TTAATTAAGCCCAGGAGTTCAAGGCTGCAGTGAGCTGTGATTGCGCCACTGCACTCCAGC 10672
Db 79172 TTAATTAAGCCCAGGAGTTCAAGGCTGCAGTGAGCTGTGATTGCGCCACTGCACTCCAGC 79231


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Qy      15032 TTAATTCTGGAATCAGAAATATTAGTCAAGGATATCAGTCTATGAAGTAAGTTTTCAATG 15091
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Qy      15212 ACTTTC--TTTTTCCTGAAGGCTCTTTGAGGTCTTTCAAGAACTCAATTCAATTCAGCAA 15269
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Qy      15270 CAATTAGGGGGTCTAAGGTATACAGACGCTGTGCAAGATGCTCCTGAGACACAAAGAGGA 15329
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Qy      15330 GGTCAAGCCCCTGCCTTCAGGCACCTCTCTATAATATAGGAGGAGAAAGAGAAGAAACAC 15389
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Qy      15390 TAATACACATAGGTAGGTGCCATTAAAAGGGTACATACATTAAAGCCAGGTGGTAGGTGT 15449
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Qy      15510 TTAAAATGGGAGATACATATATATGTATTTATGTATGTATATATGTATGTACATATACAC 15569
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Qy      15810 ATAGACATAAATATGTATATATGTGTATATAGACATAAATATGTATATATGTGTATATAG 15869
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Qy      15870 ACATAAATATGTATATATGTGTATATAGACATAAATATGTATATATGTGTATATAGACAT 15929
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Qy      16030 -------TGTATATAGACATAAATATGTATATATGTGTGTATATAATAATGTGTGT-CAT 16081
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Qy      16082 ATACACACATATATACATACATAAACATTCTGCATTATACCATTCACTTTGTAACCCATC 16141
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Qy      16382 ACCACTGCTCATCTTTTCTGCTGCCACAACTCCAGTCCAAGCCACAAACCTCTCTCTCCT 16441
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Qy      16442 GGACTCCTGCGGGGAGTTCCTTTCTCTCCCTGCATGAGTCTATTCTCCGCACAACTGGCA 16501
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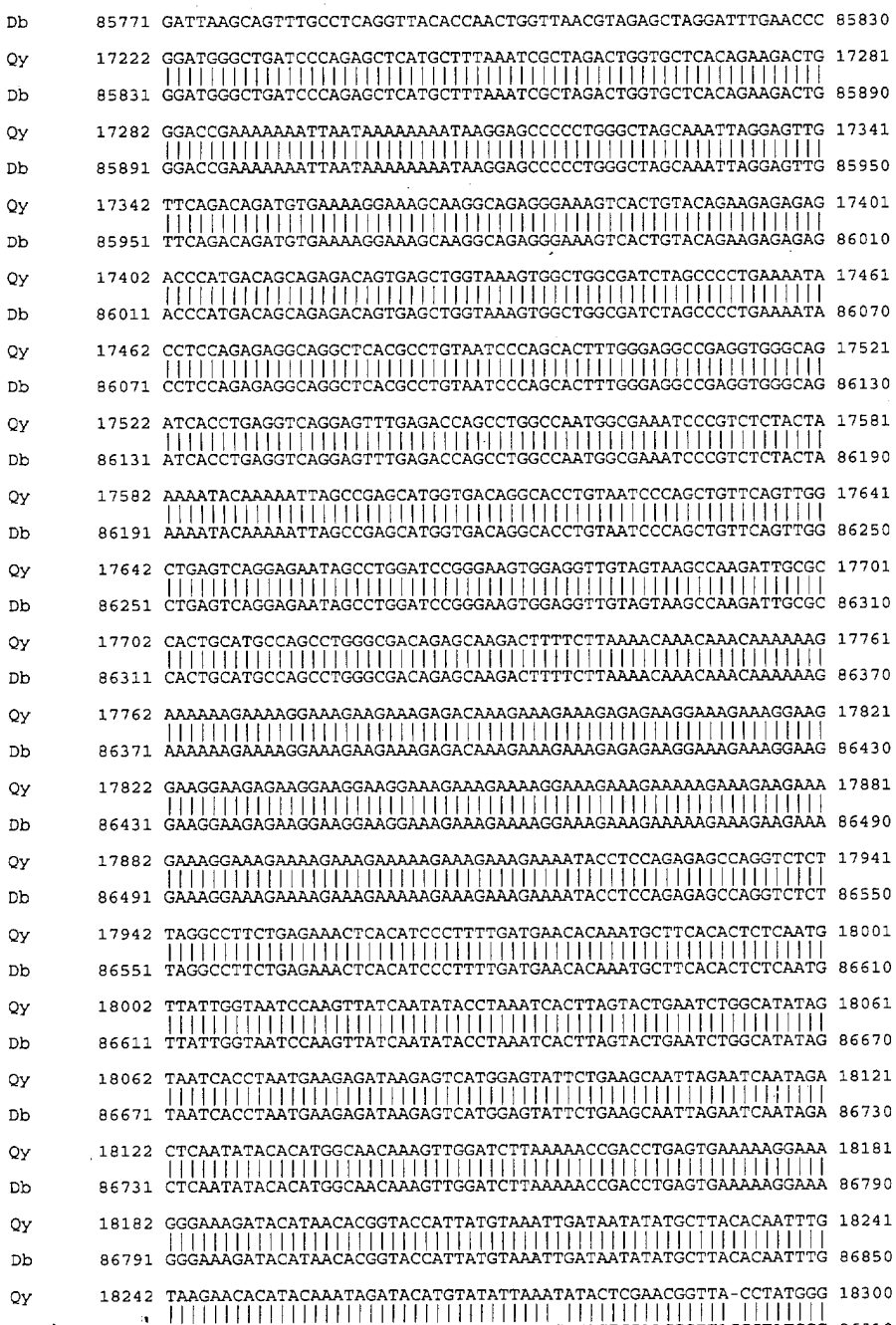
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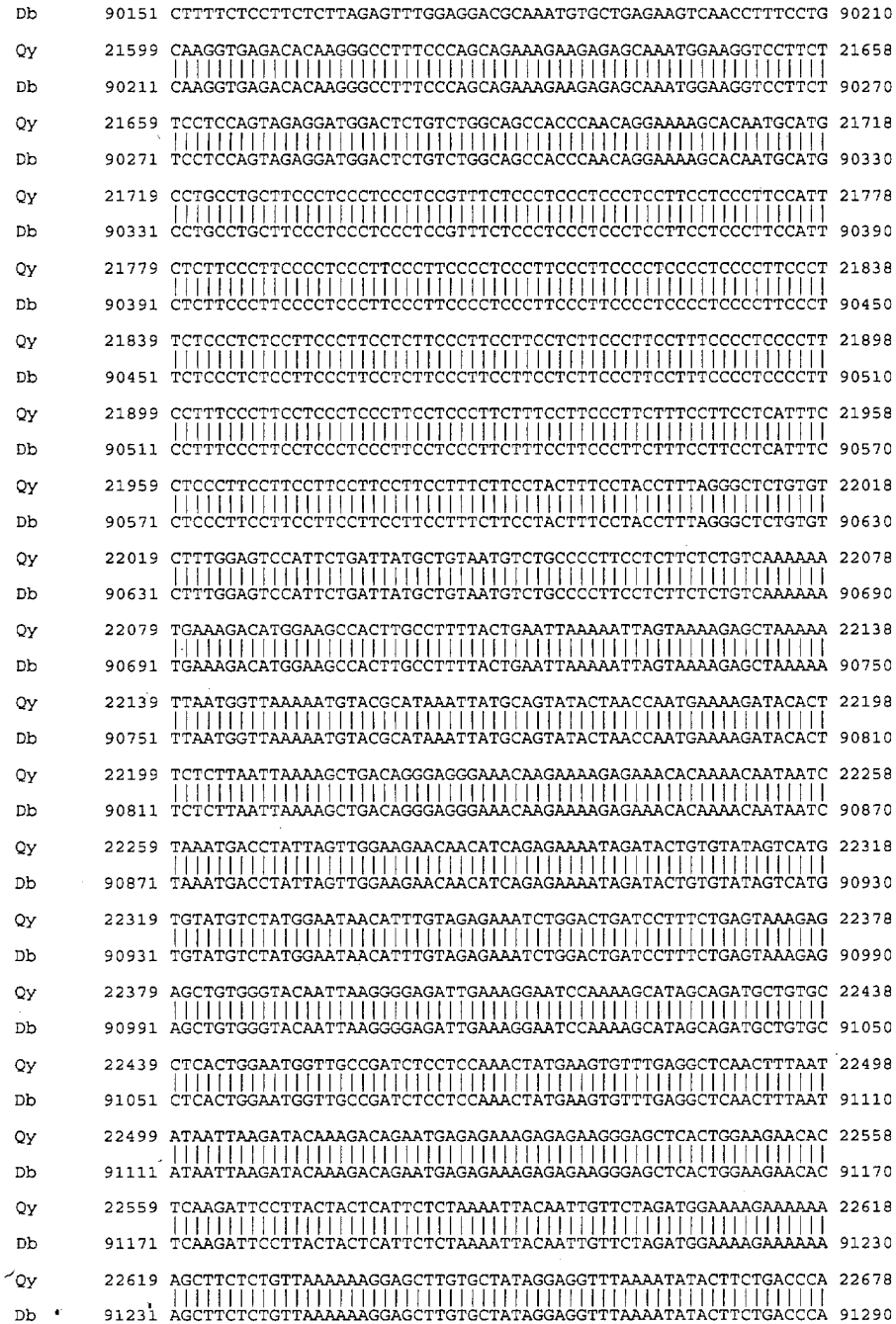
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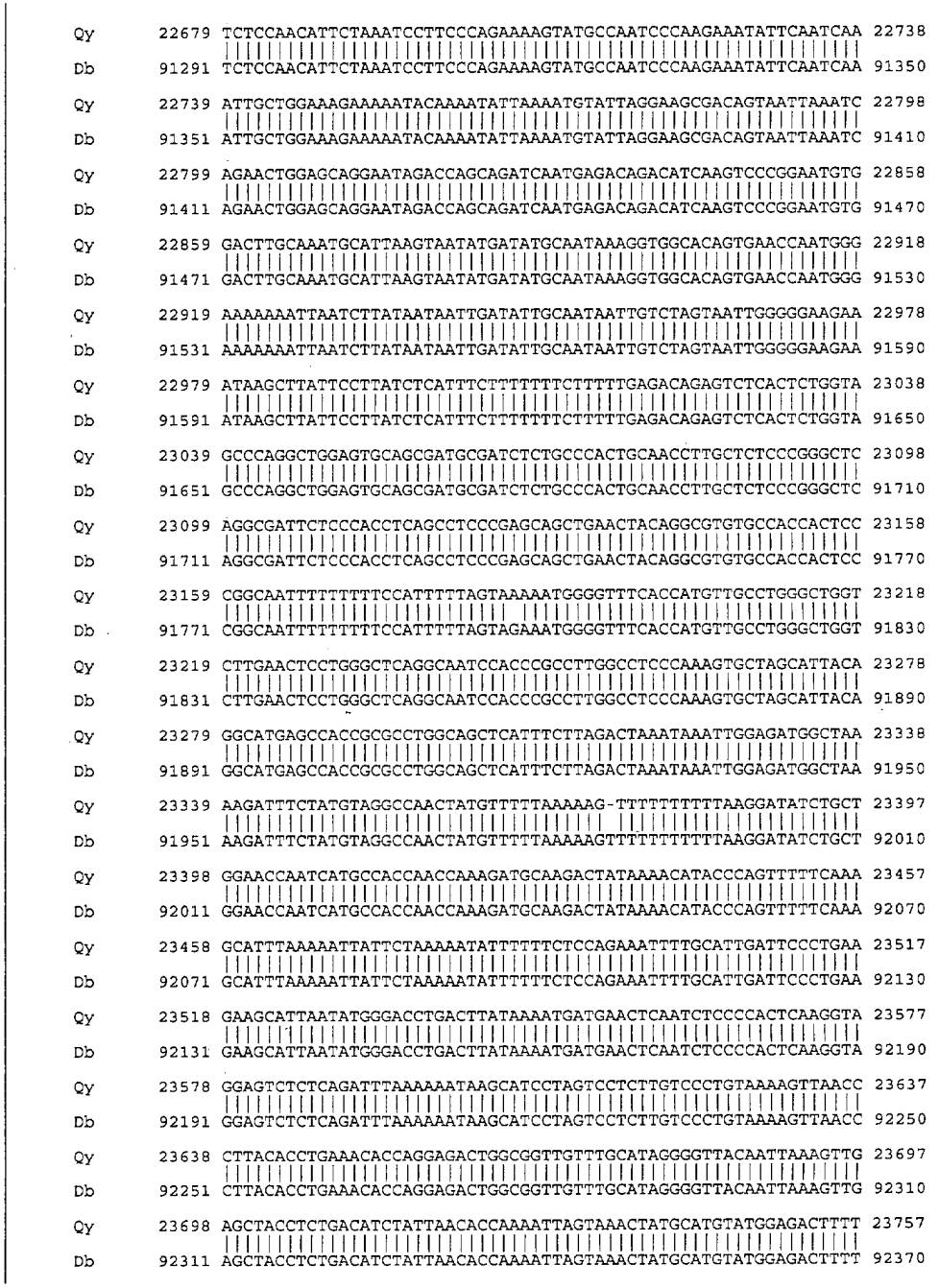
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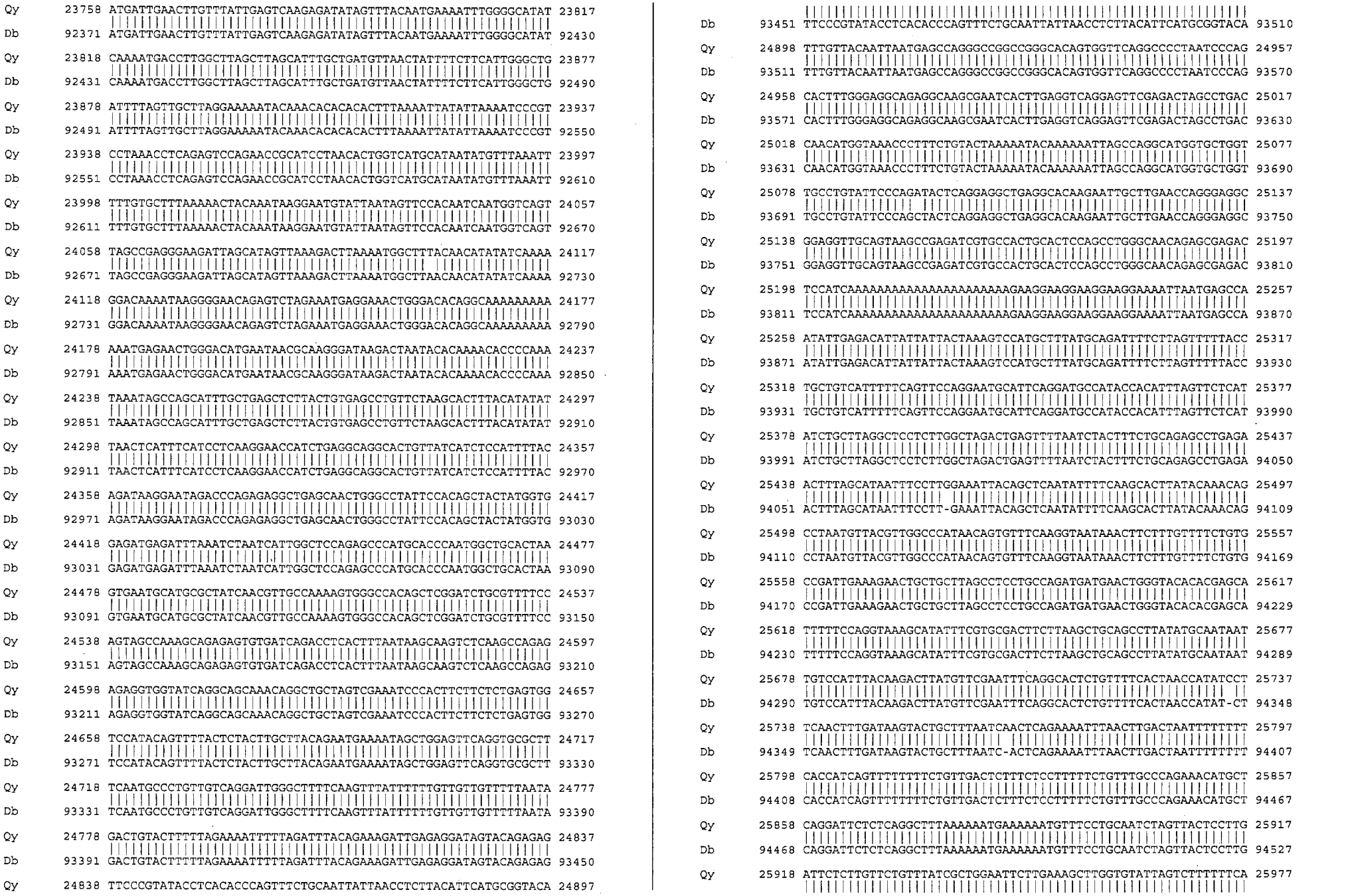
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Qy      21479 CTGGCAGCTTTCACAAGAAGGGCTTCTGACTCAAGGATGTTTCCATCTTTGCCAGGTCGC 21538
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Qy      21539 CTTTTCTCCTTCTCTTAGAGTTTGGAGGACGCAAATGTGCTGAGAAGTCAACCTTTCCTG 21598
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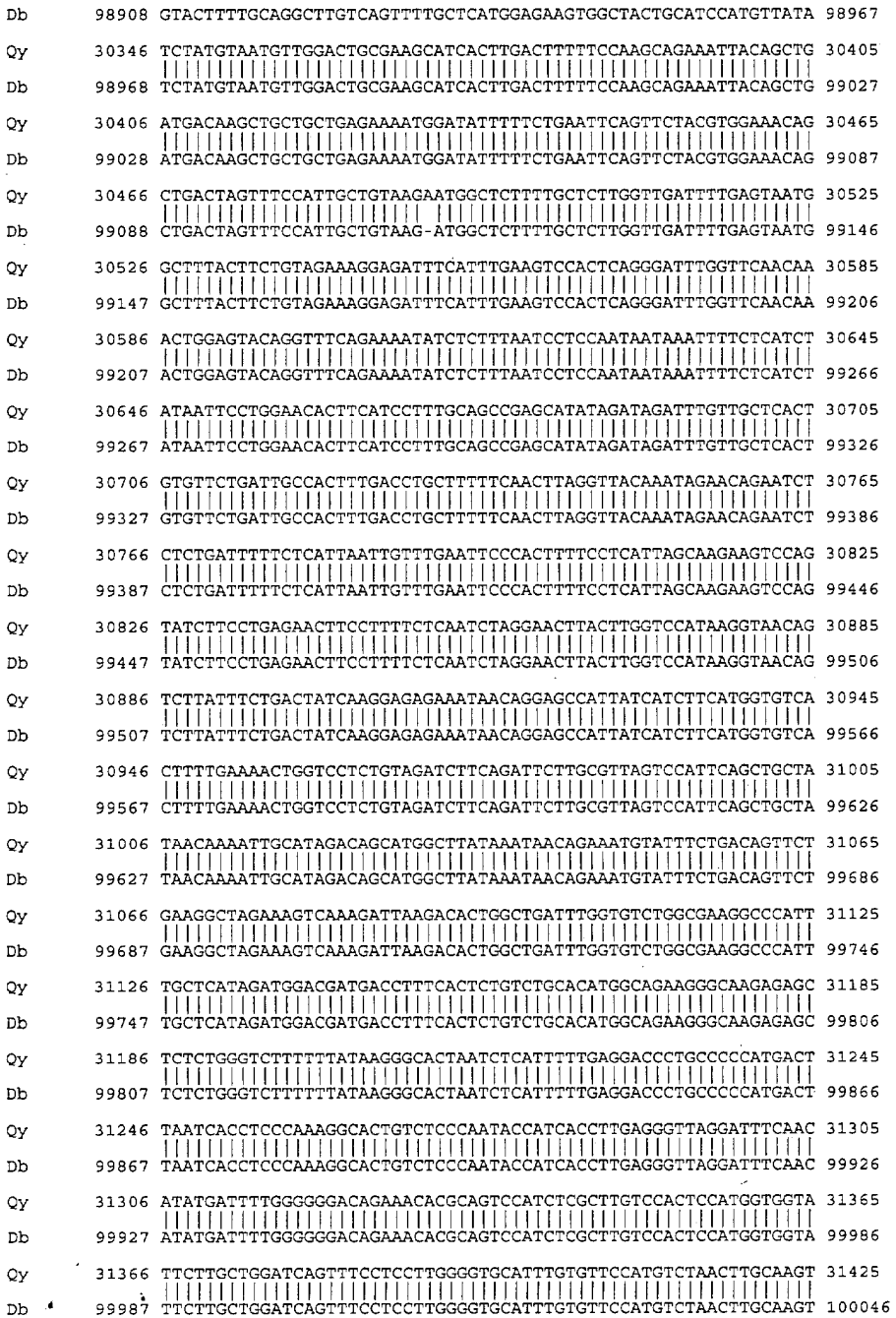

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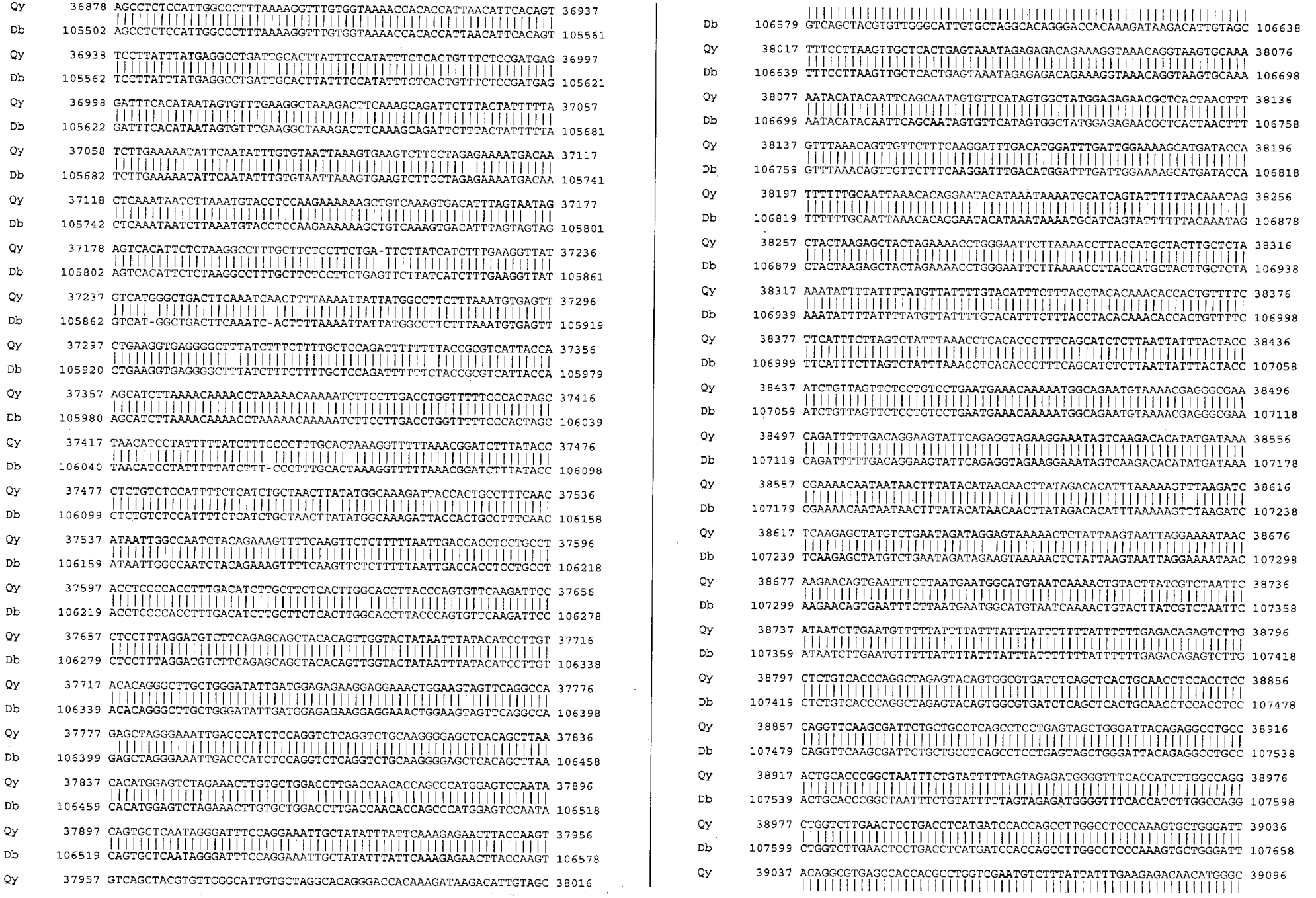

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Db 102743 GTGGTGGGAAGCTGGGTCTCCTAAGGAGGTTTTGACAAAAGCAGTCATGGAGCGGGCTTA 102802
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Db 102803 GAAATCACAGTTGGGGACAGGGTAGAGTTCCTCGGGATATAGAGGATGAGATTAGAAGAG 102862
Qy 34241 GTTCCAACTAGGGTAGTGTGGAGAAAAGCACTATTGACCCAAAAAGGAAGGAGAATGTGG 34300
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RESULT 4
AF222856
LOCUS       AF222856               69058 bp    DNA     linear   PRI 17-JUL-2000
DEFINITION  Homo sapiens clone PnC chromosome 10 map 10q25.2 genomic sequence.
ACCESSION   AF222856
VERSION     AF222856.1  GI:9246846
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 69058)
  AUTHORS   Barry,A.E., Bateman,M., Howman,E.V., Cancilla,M.R., Tainton,K.M.,
            Irvine,D.V., Saffery,R. and Choo,K.H.
  TITLE     The 10q25 neocentromere and its inactive progenitor have identical
            primary nucleotide sequence: further evidence for epigenetic
            modification
  JOURNAL   Genome Res. 10 (6), 832-838 (2000)
  MEDLINE   20314874
   PUBMED   10854414
REFERENCE   2  (bases 1 to 69058)
  AUTHORS   Barry,A.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JAN-2000) Chromosome Research Unit, The Murdoch
            Institute, 10th Floor, Royal Childrens Hospital, Flemington Rd.,
            Parkville,, Melbourne, Victoria 3052, Australia
  REMARK    Human genomic sequence from 10q25.2, clonelib=PnC
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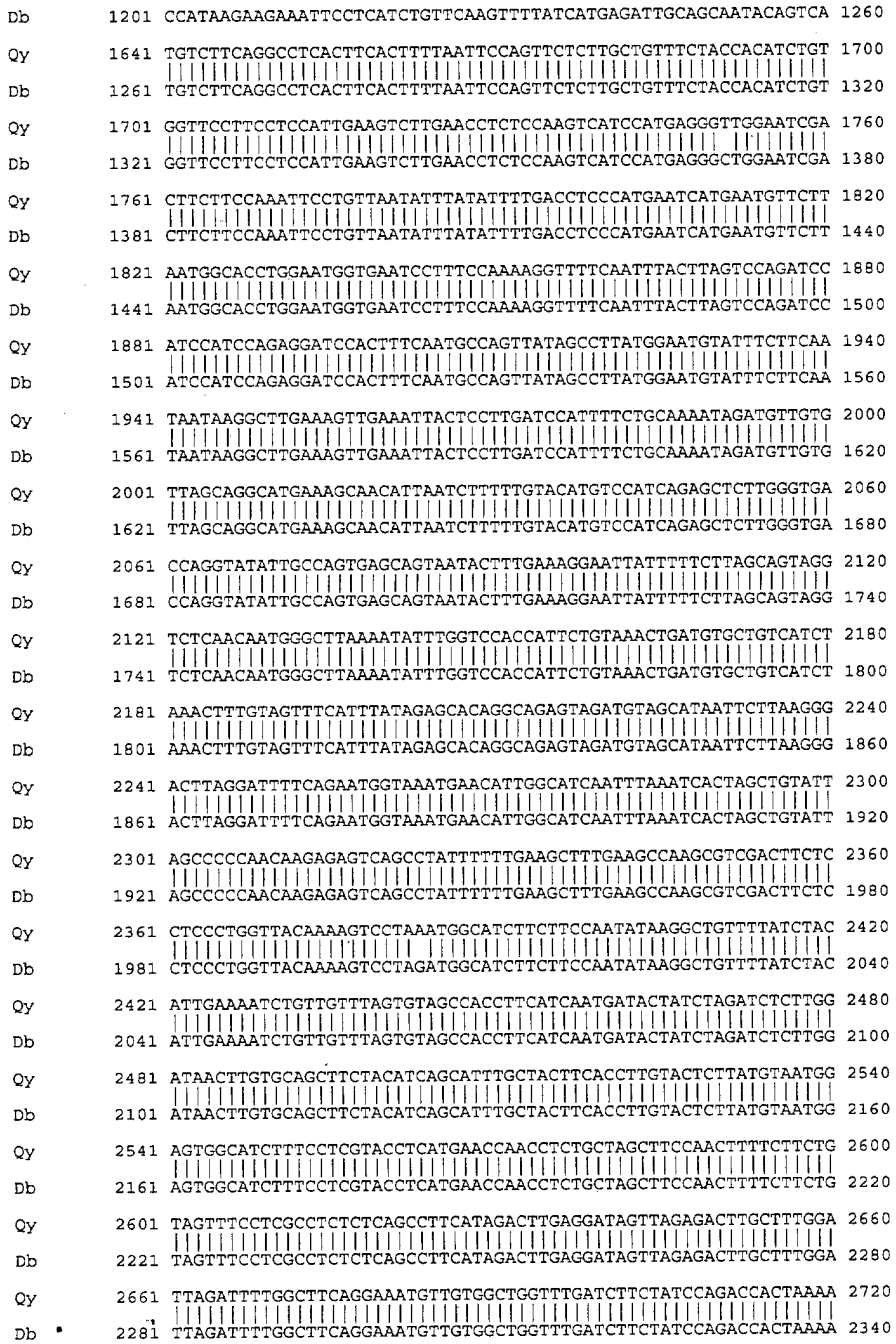
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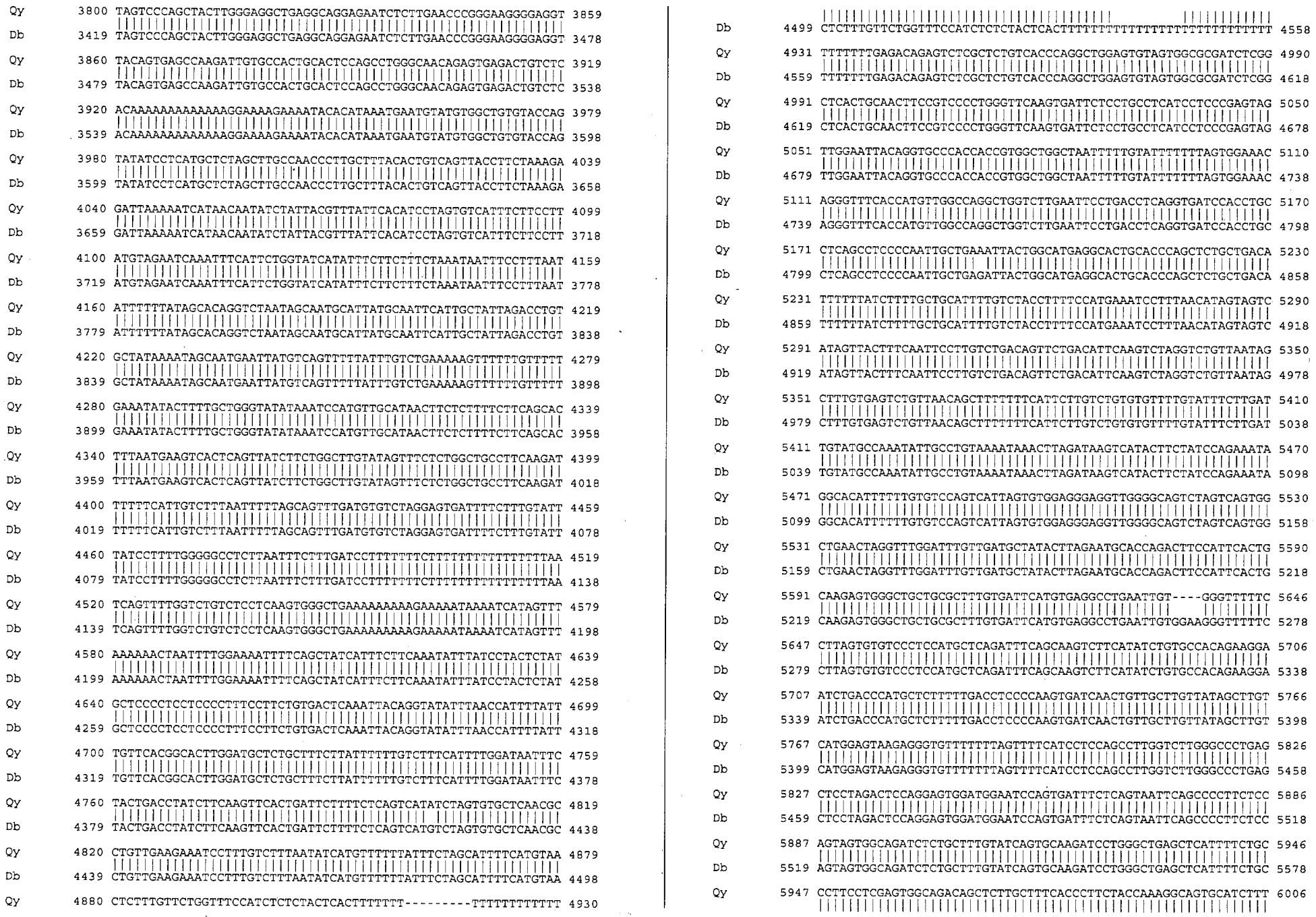
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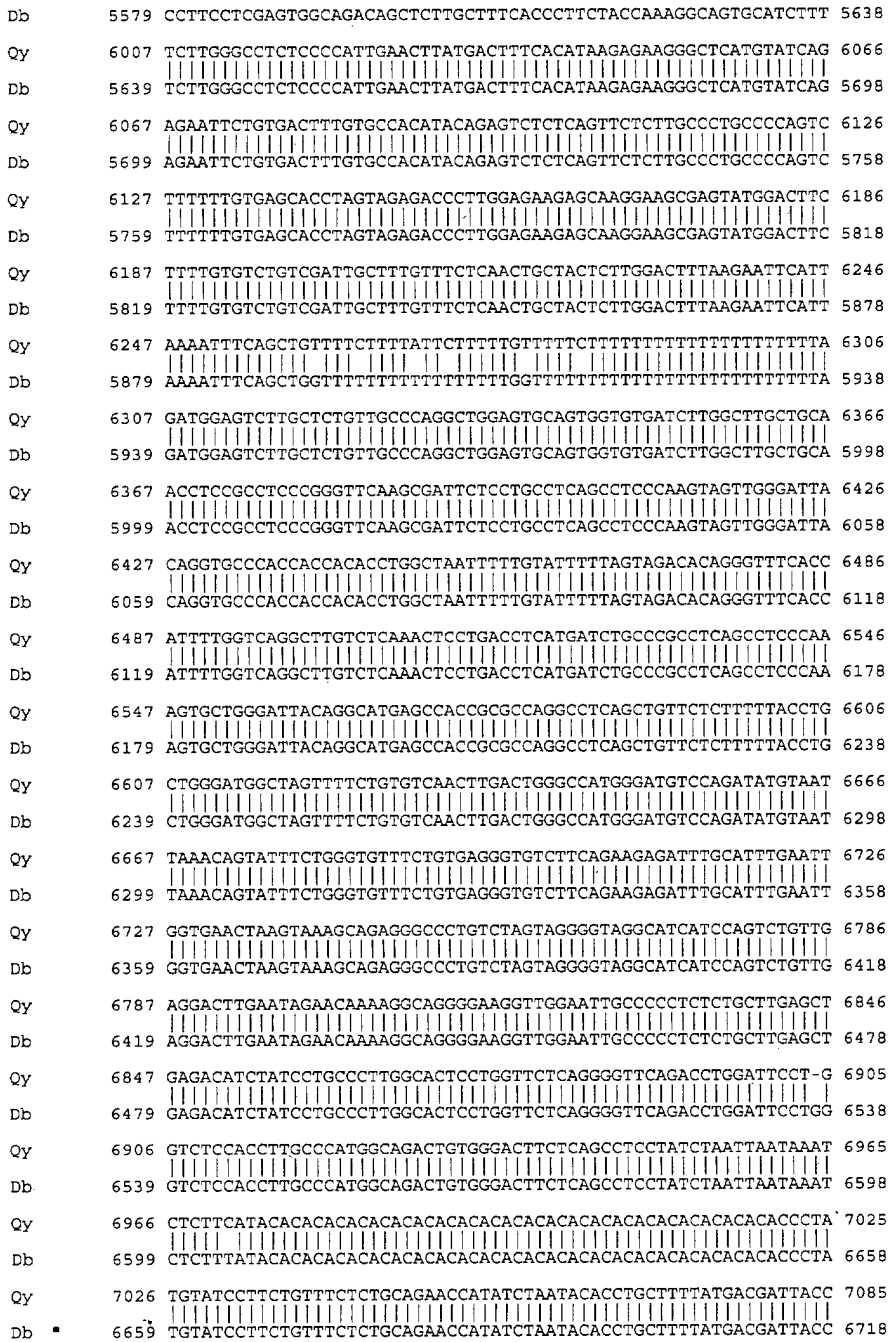
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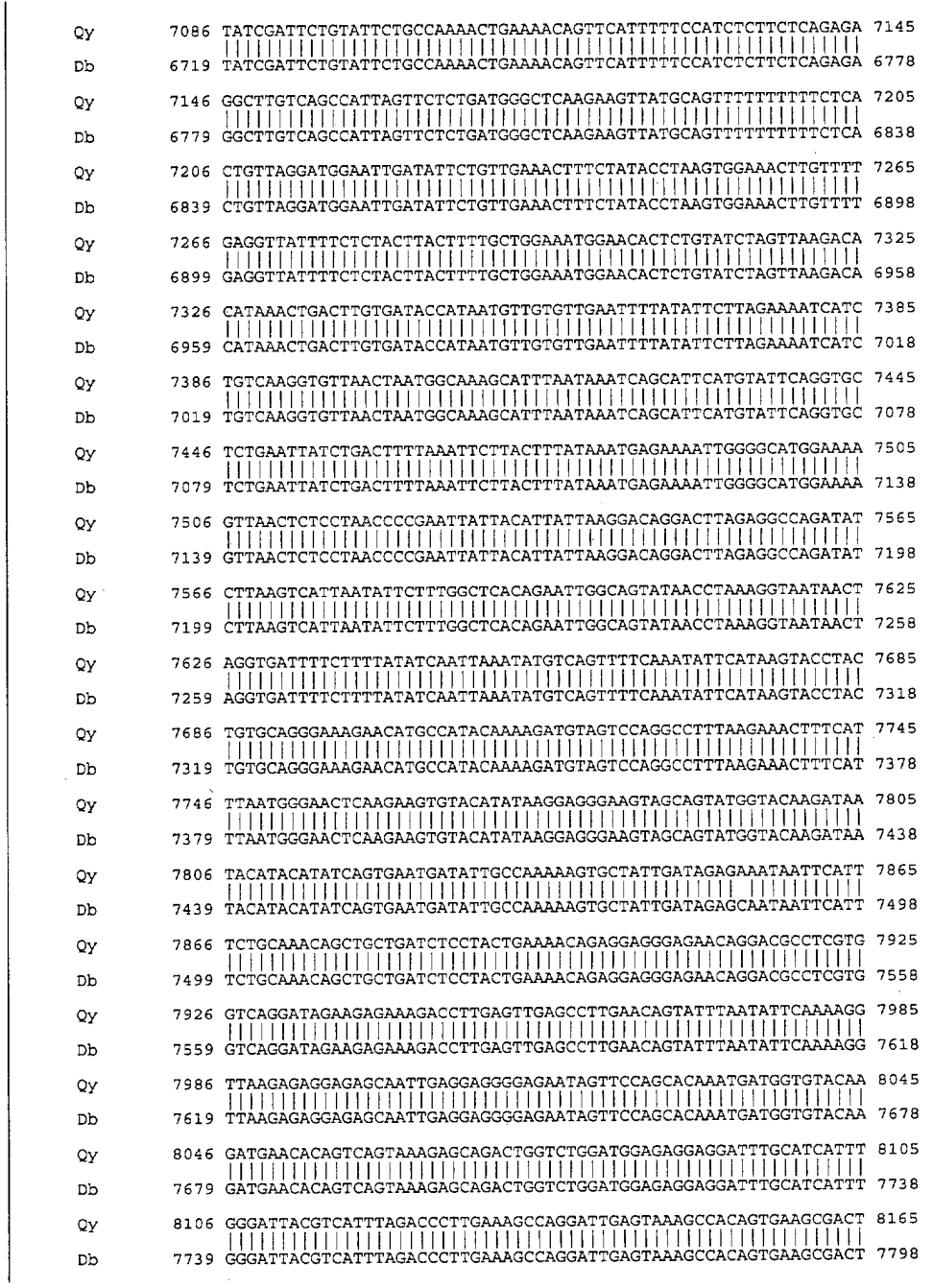
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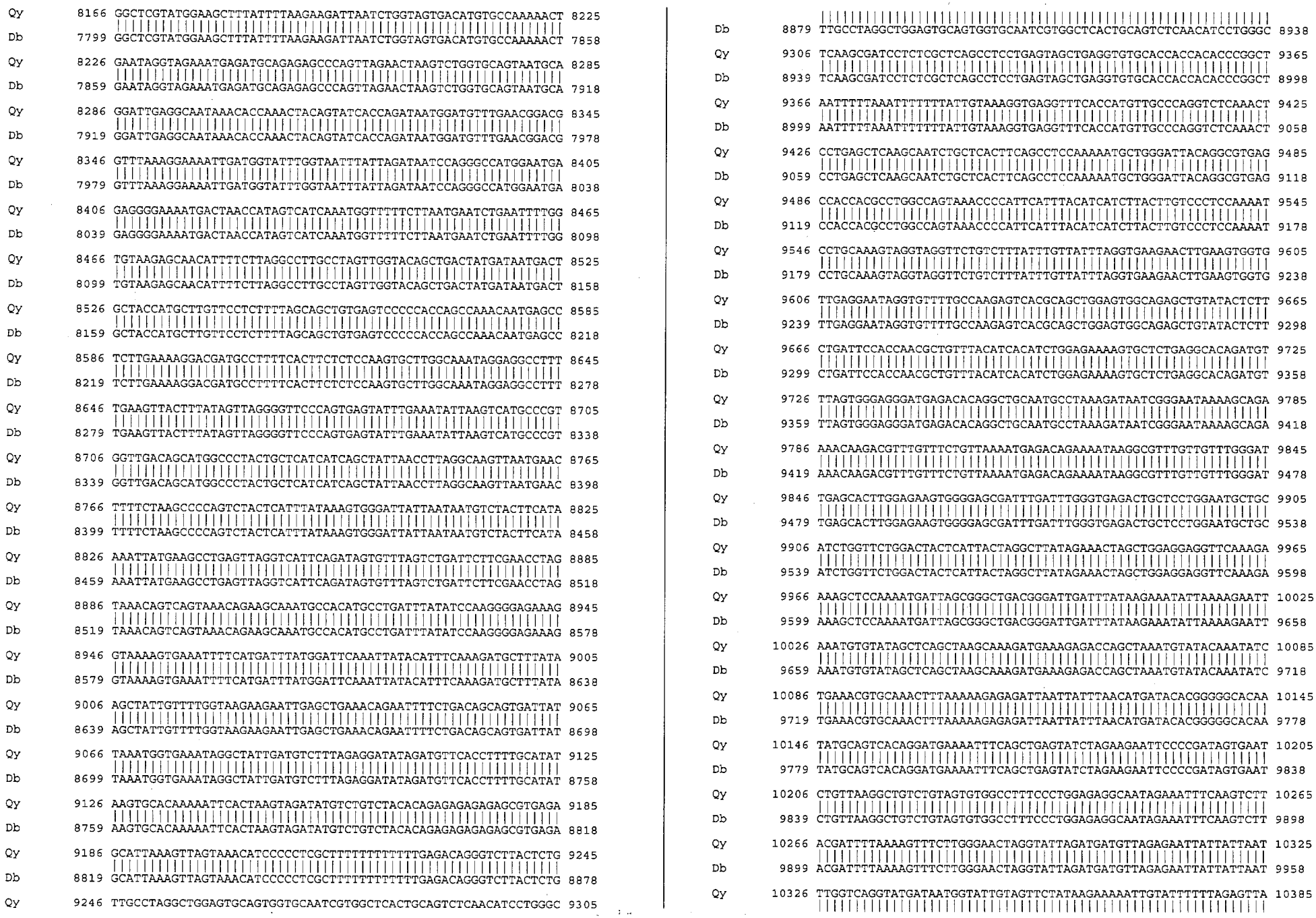
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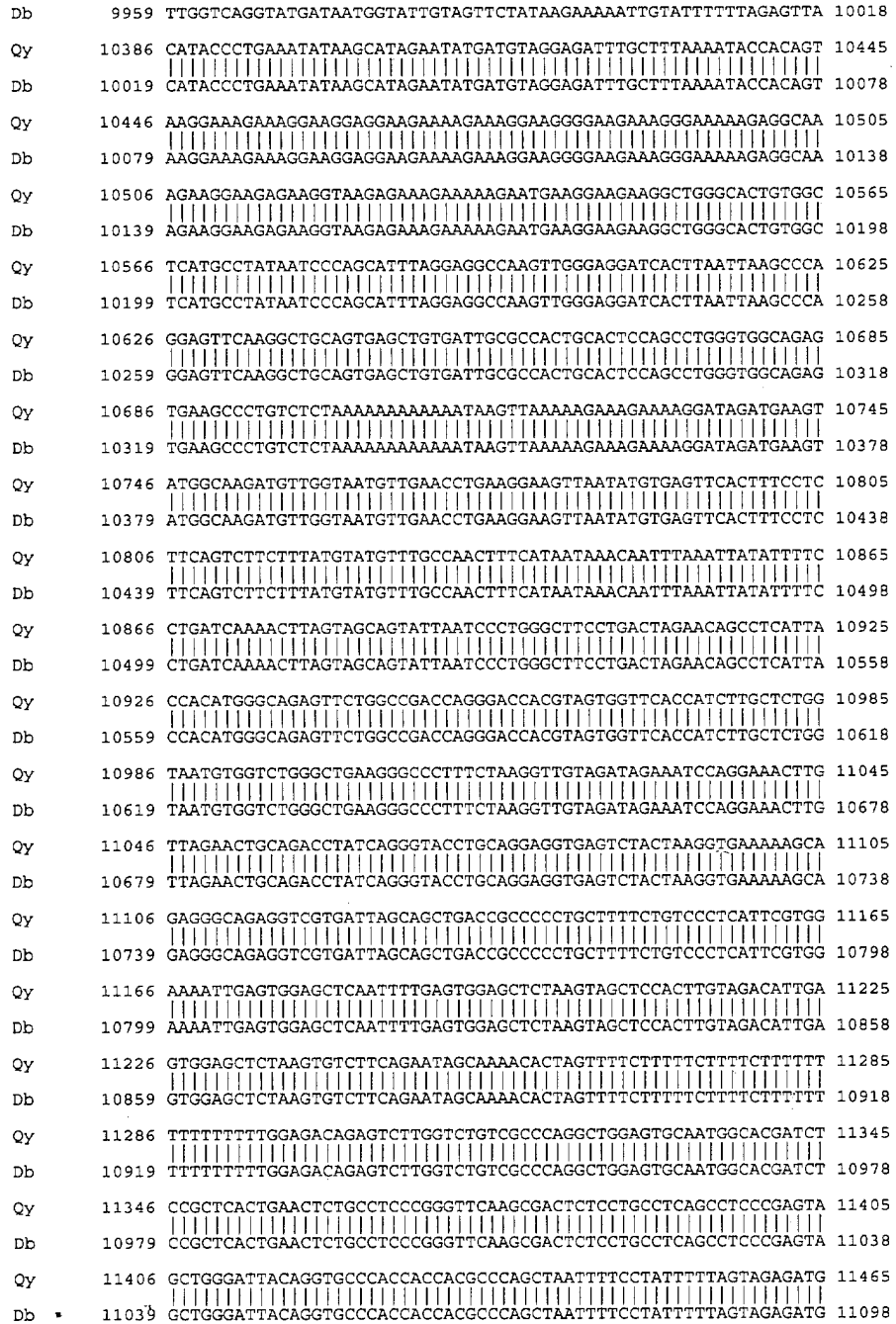

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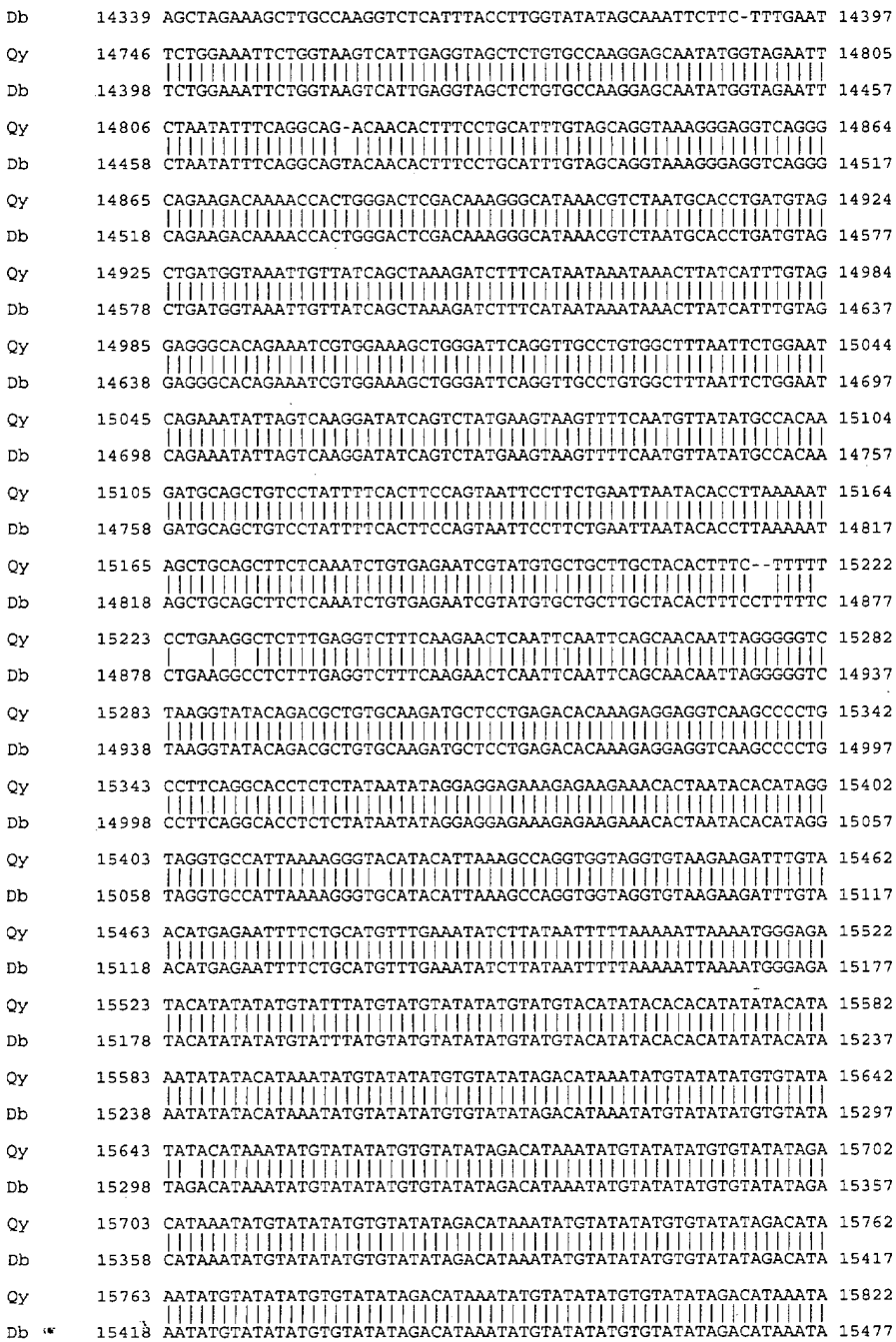

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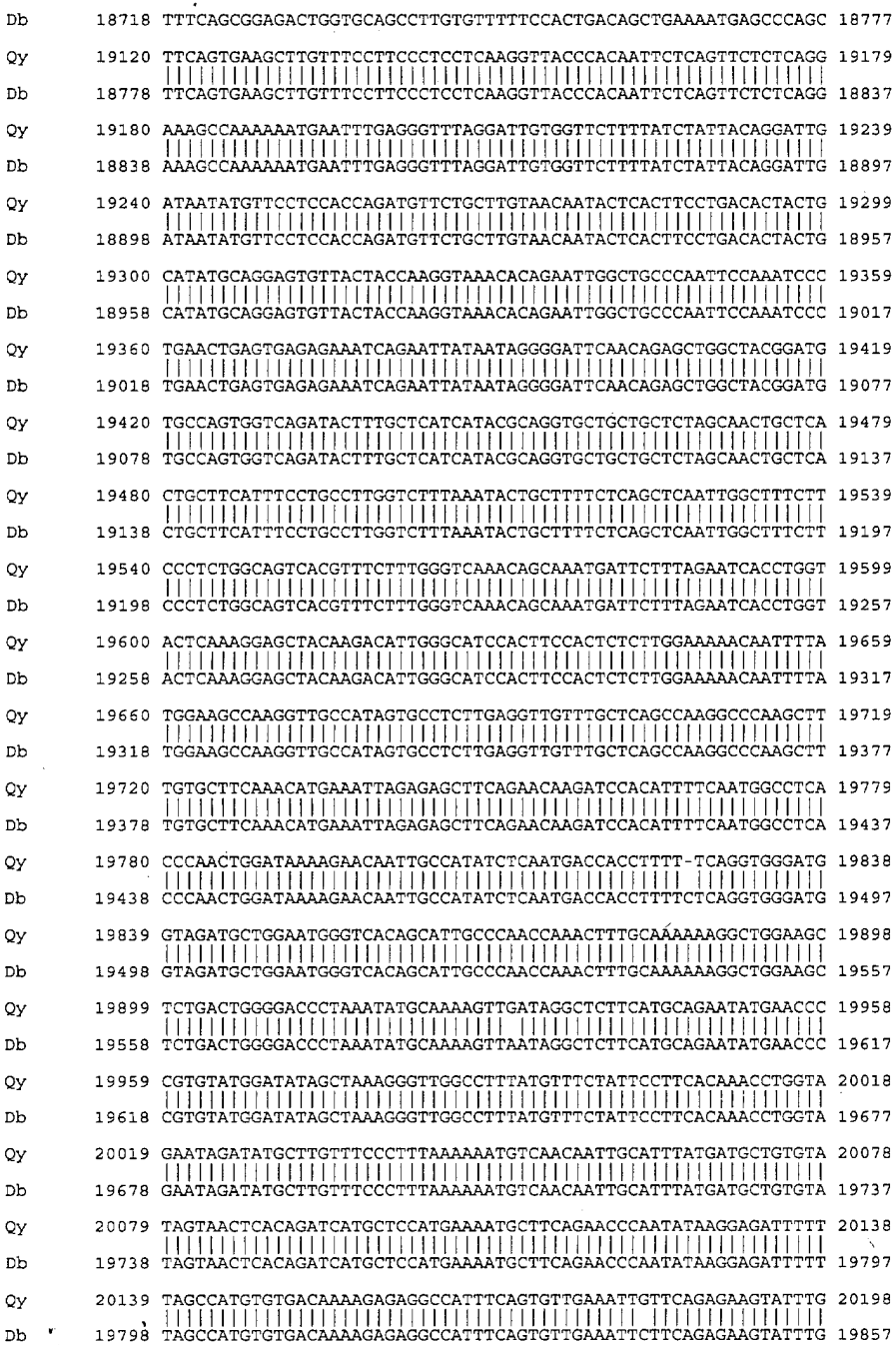

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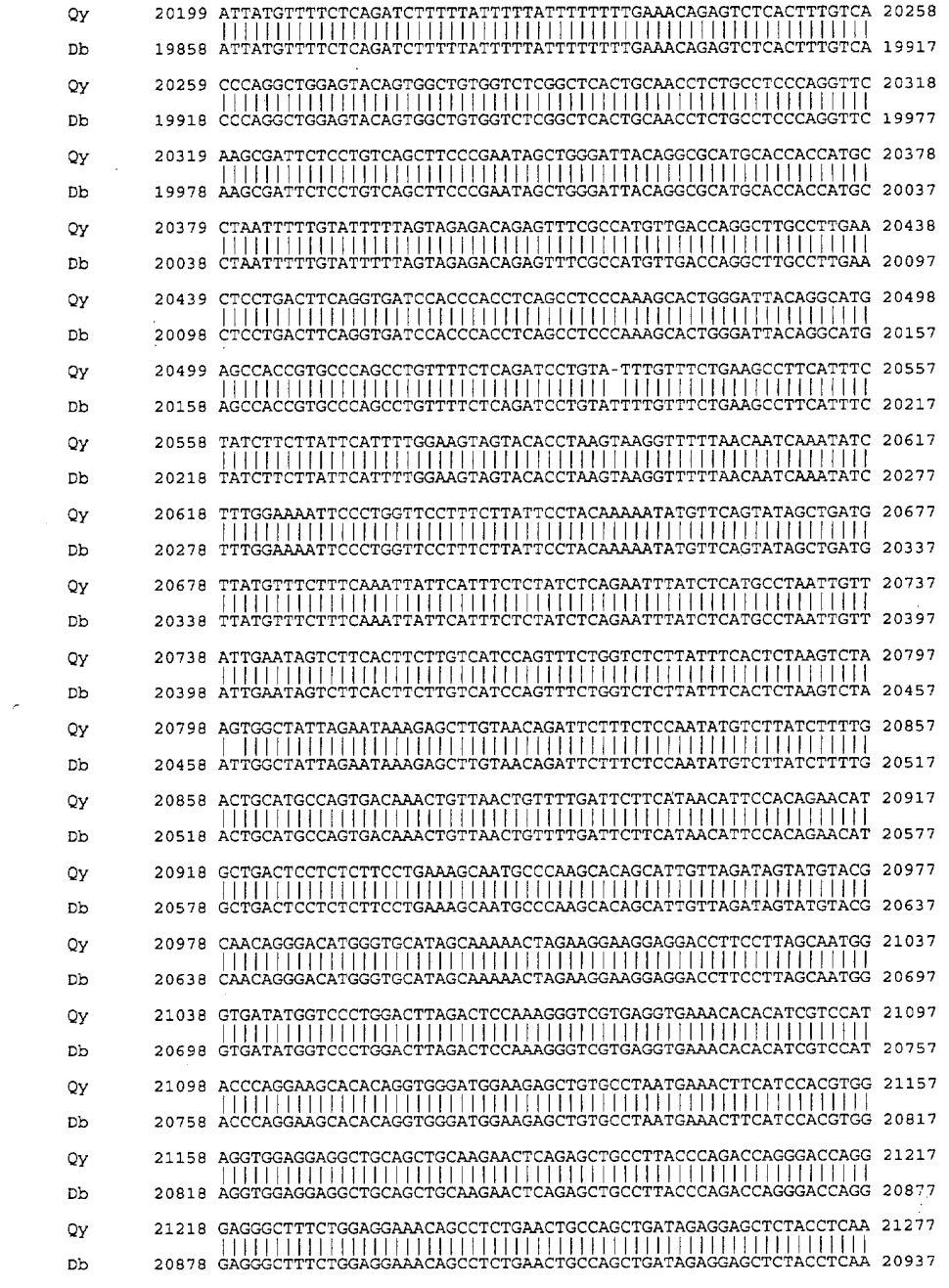

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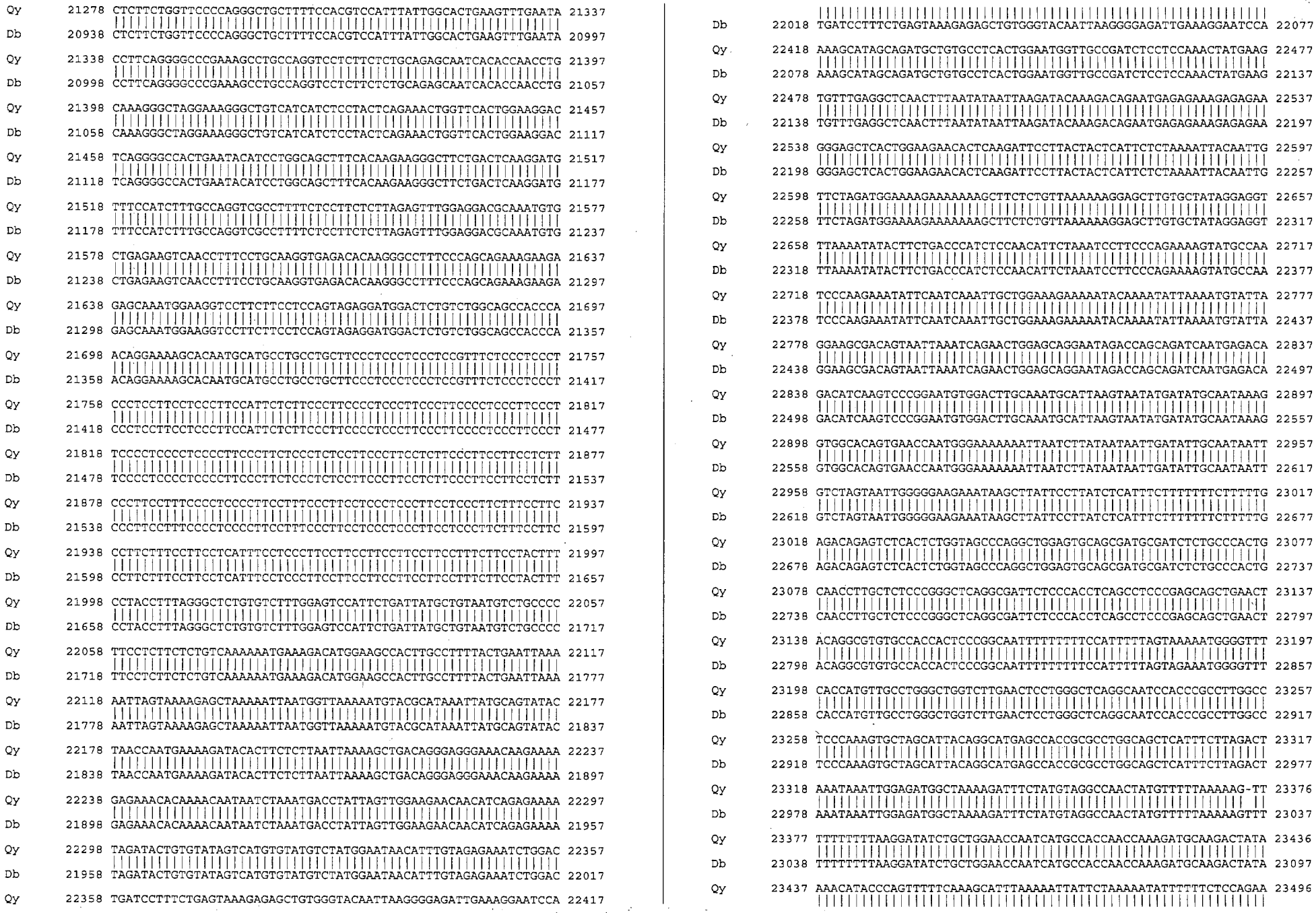


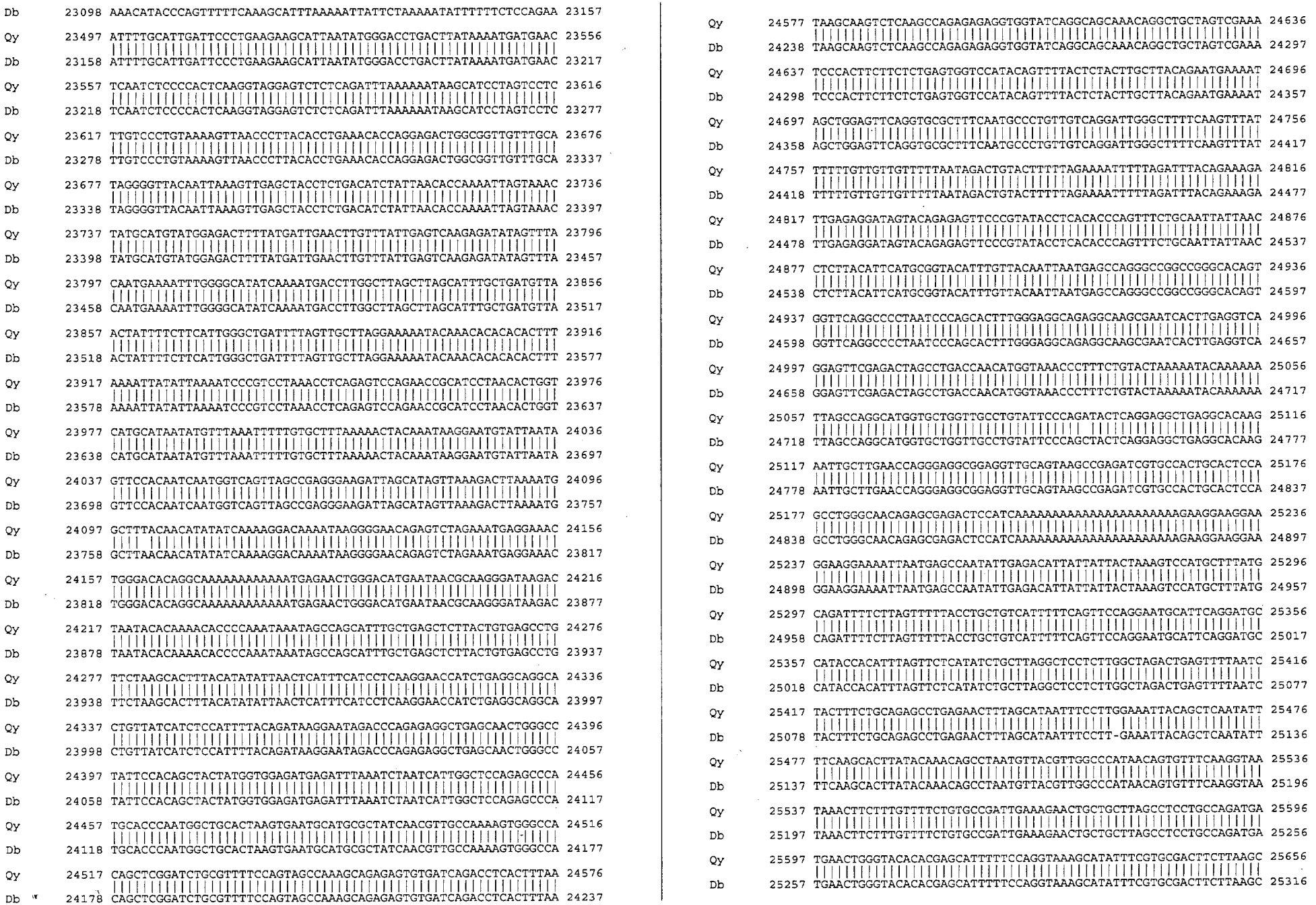

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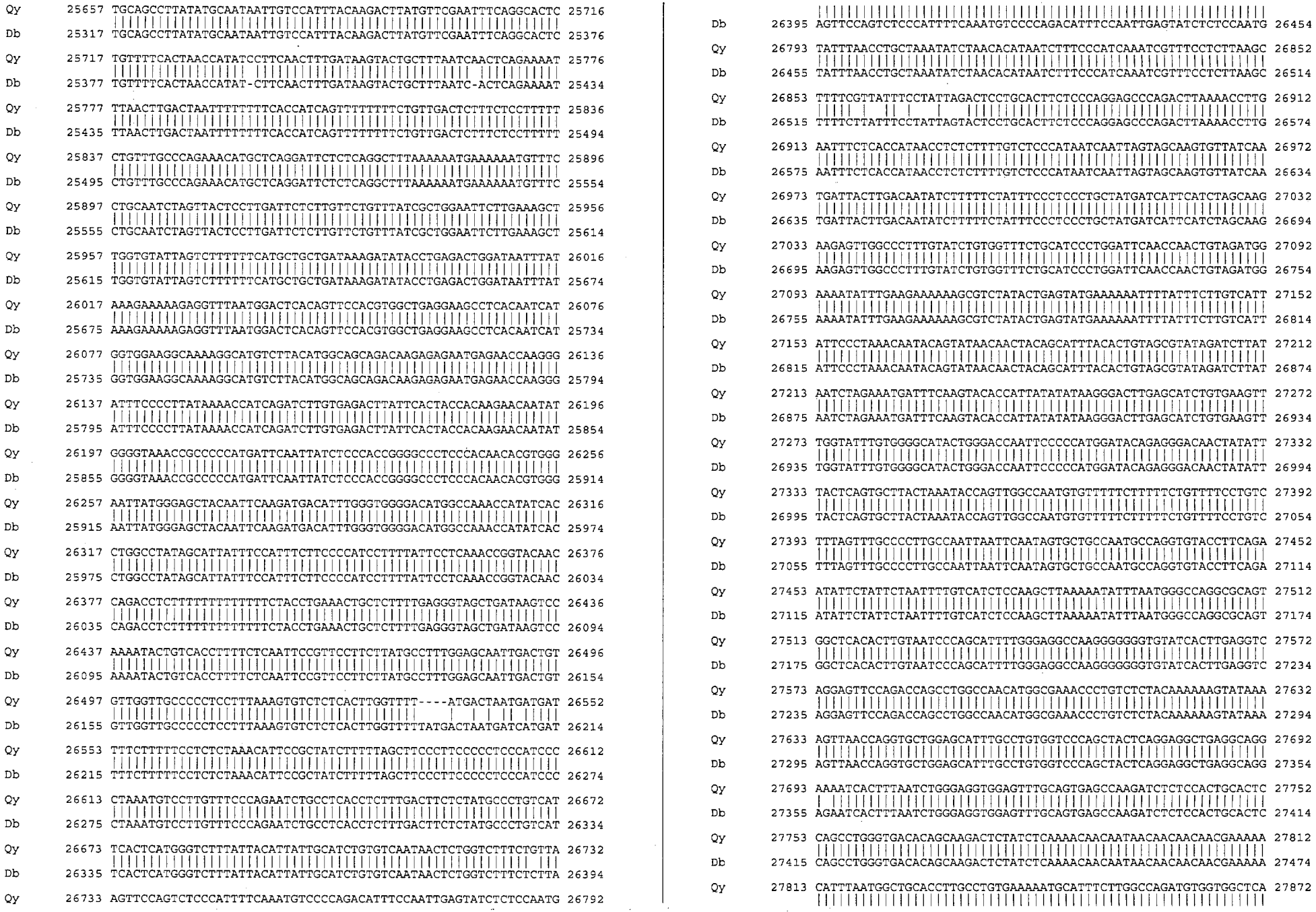

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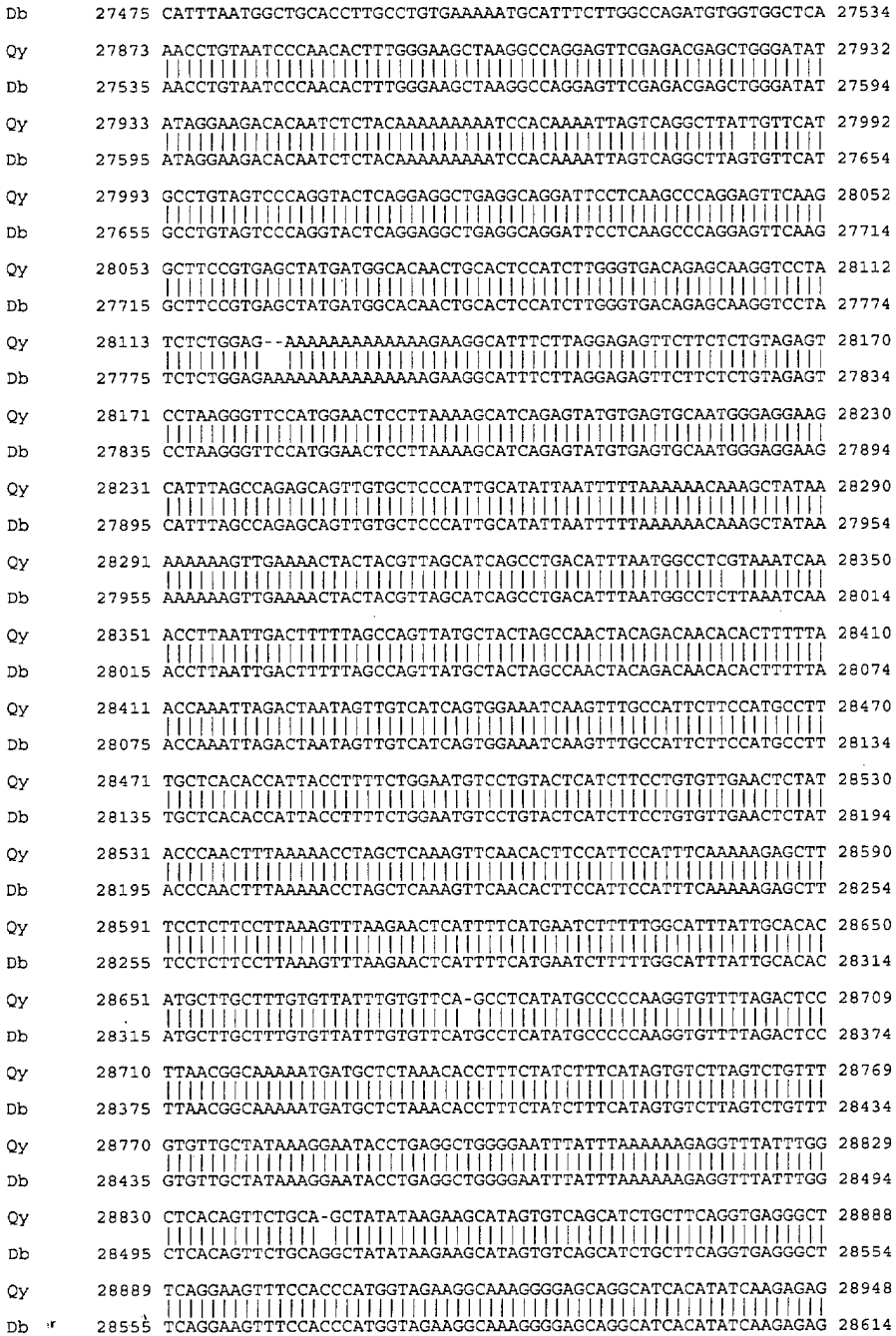

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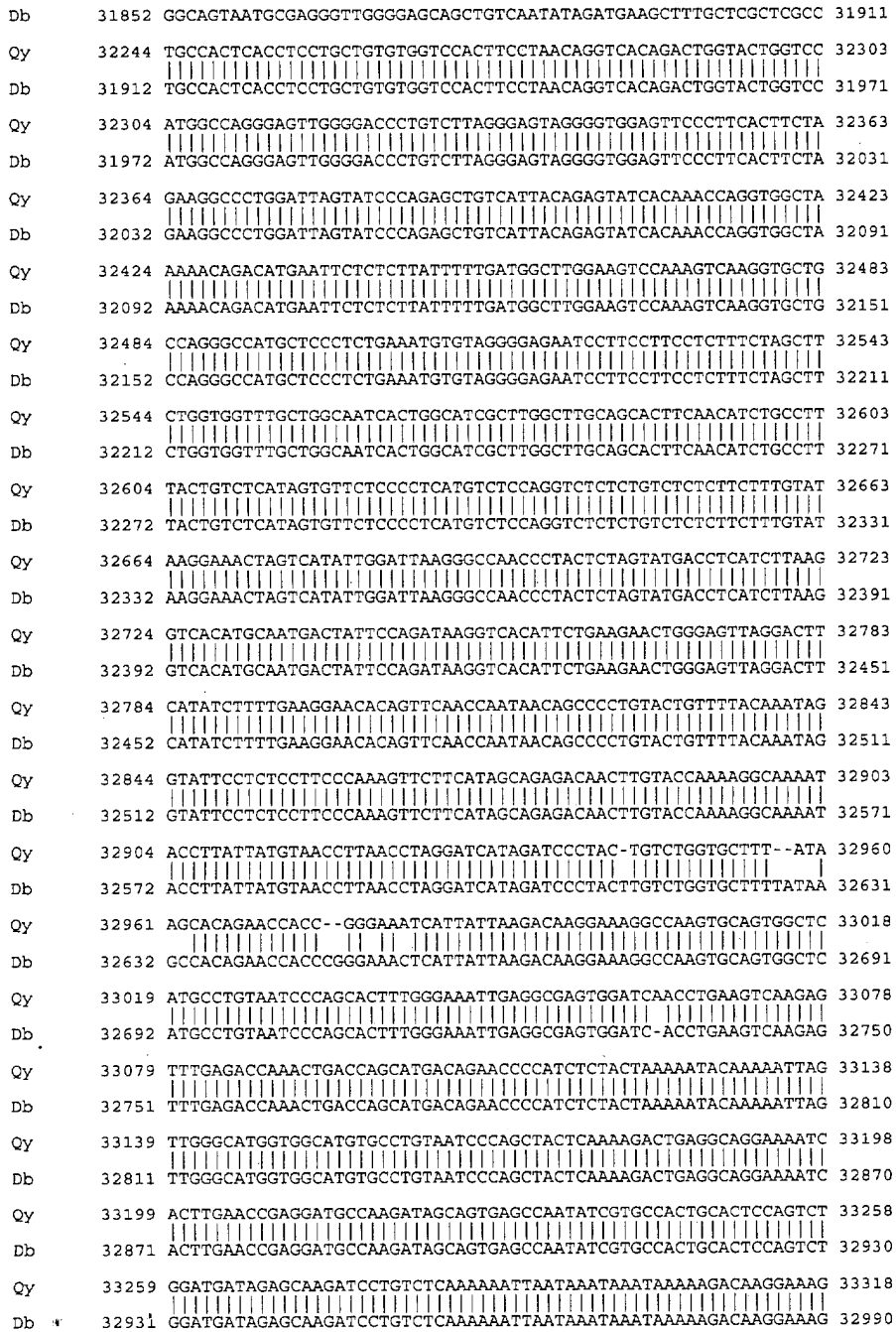
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31672 TTGTTTTCCTGCAACTAGACAGTCCCATCTGGGGGCAATGGGAGATAGTGACAGATCATC 31731

Qy      32064 AAGCATTAGATTCTCATAAGGAGTGCTCAGCCTAGATCCCCGGCATGTGCAGTTCACAAT 32123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31732 AAGCATTAGATTCTCATAAGGAGTGCTCAGCCTAGATCCCCGGCATGTGCAGTTCACAAT 31791

Qy      32124 AGGATTTGCTCACCTATGAGAATCTAATGCCACTGCTGATCTGACAGGAGGTGGAGCTCG 32183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31792 AGGATTTGCTCACCTATGAGAATCTAATGCCACTGCTGATCTGACAGGAGGTGGAGCTCG 31851

Qy      32184 GGCAGTAATGCGAGGGTTGGGGAGCAGCTGTCAATATAGATGAAGCTTTGCTCGCTCGCC 32243
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Db 31852 GGCAGTAATGCGAGGGTTGGGGAGCAGCTGTCAATATAGATGAAGCTTTGCTCGCTCGCC 31911
Qy 32244 TGCCACTCACCTCCTGCTGTGTGGTCCACTTCCTAACAGGTCACAGACTGGTACTGGTCC 32303
Db 31912 TGCCACTCACCTCCTGCTGTGTGGTCCACTTCCTAACAGGTCACAGACTGGTACTGGTCC 31971
Qy 32304 ATGGCCAGGGAGTTGGGGACCCTGTCTTAGGGAGTAGGGGTGGAGTTCCCTTCACTTCTA 32363
Db 31972 ATGGCCAGGGAGTTGGGGACCCTGTCTTAGGGAGTAGGGGTGGAGTTCCCTTCACTTCTA 32031
Qy 32364 GAAGGCCCTGGATTAGTATCCCAGAGCTGTCATTACAGAGTATCACAAACCAGGTGGCTA 32423
Db 32032 GAAGGCCCTGGATTAGTATCCCAGAGCTGTCATTACAGAGTATCACAAACCAGGTGGCTA 32091
Qy 32424 AAAACAGACATGAATTCTCTCTTATTTTTGATGGCTTGGAAGTCCAAAGTCAAGGTGCTG 32483
Db 32092 AAAACAGACATGAATTCTCTCTTATTTTTGATGGCTTGGAAGTCCAAAGTCAAGGTGCTG 32151
Qy 32484 CCAGGGCCATGCTCCCTCTGAAATGTGTAGGGGAGAATCCTTCCTTCCTCTTTCTAGCTT 32543
Db 32152 CCAGGGCCATGCTCCCTCTGAAATGTGTAGGGGAGAATCCTTCCTTCCTCTTTCTAGCTT 32211
Qy 32544 CTGGTGGTTTGCTGGCAATCACTGGCATCGCTTGGCTTGCAGCACTTCAACATCTGCCTT 32603
Db 32212 CTGGTGGTTTGCTGGCAATCACTGGCATCGCTTGGCTTGCAGCACTTCAACATCTGCCTT 32271
Qy 32604 TACTGTCTCATAGTGTTCTCCCCTCATGTCTCCAGGTCTCTCTGTCTCTCTTCTTTGTAT 32663
Db 32272 TACTGTCTCATAGTGTTCTCCCCTCATGTCTCCAGGTCTCTCTGTCTCTCTTCTTTGTAT 32331
Qy 32664 AAGGAAACTAGTCATATTGGATTAAGGGCCAACCCTACTCTAGTATGACCTCATCTTAAG 32723
Db 32332 AAGGAAACTAGTCATATTGGATTAAGGGCCAACCCTACTCTAGTATGACCTCATCTTAAG 32391
Qy 32724 GTCACATGCAATGACTATTCCAGATAAGGTCACATTCTGAAGAACTGGGAGTTAGGACTT 32783
Db 32392 GTCACATGCAATGACTATTCCAGATAAGGTCACATTCTGAAGAACTGGGAGTTAGGACTT 32451
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Db 32632 GCCACAGAACCACCCGGGAAACTCATTATTAAGACAAGGAAAGGCCAAGTGCAGTGGCTC 32691
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Db 33230 G-AAAAAAAAAAAAAAAAAAAAGCTGGGTGTGTTGGCTTATGCCTGTAGTCTCAGCTACC 33288
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Qy 34219 ATAGAGGATGAGATTAGAAGAGGTTCCAACTAGGGTAGTGTGGAGAAAAGCACTATTGAC 34278
Db 33889 ATAGAGGATGAGATTAGAAGAGGTTCCAACTAGGGTAGTGTGGAGAAAAGCACTATTGAC 33948
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Db 34008 GGTGATTTTTCTAATGCAGAGTTGTGGGAGGTGGAGTGCAGGGAGCCAGGCTGGGTGGCT 34067

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Qy      34399 GTGCTGATGTGATTAAGCACTTACTGACTGCCAGGCAATGGGCTAAGTACCTGAGATGCT 34458
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Db      34068 GTGCTGATGTGATTAAGCACTTACTGACTGCCAGGCAATGGGCTAAGTACCTGAGATGCT 34127

Qy      34459 TTGTCTGTTATCCCTCCCGAAACCCCTCTGAGCAGGTGCAGTTATTATTCTCACTTCACA 34518
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Qy      34519 GATAAGGAAATTGAGGCACAGAGAA-TTGAGTAACTTACCCAAGGTGACATAGCTCATAT 34577
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db      34188 GATAAGGAAATTGAGGCACAGAGAAGTTGAGTAACTTACCCAAGGTGACATAGCTCATAT 34247

Qy      34578 ATGGTAAAGCAGGCTTTGAACTCAGTCTAGCTCCCGAACCTAAGCTTGTAACTACTATGC 34637
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Qy      34638 TTTTCCCAAAAAAAGGGGGCTGGCACAAAAAGAGCTGA-GGGGGCTGGGCATGGTGGCTC 34696
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Qy      34697 ATGCCTGTAATCCCAGCACTTCGGGAGACTGAGGCAGGTGGTTCACCAGAGTTCAGGAGT 34756
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Db      34368 ATGCCTGTAATCCCAGCACTTCGGGAGACTGAGGCAGGTGGTTCACCAGAGGTCAGGAGT 34427

Qy      34757 TCGAGACCAGCCTGGTCAACATGGTGAAGCCCTGTCTCTACTAAAAATACAAAAATTAGC 34816
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Db      34428 TCGAGACCAGCCTGGTCAACATGGTGAAGCCCTGTCTCTACTAAAAATACAAAAATTAGC 34487

Qy      34817 TGGGTGTGGTGGTGTGCACCTGTAGTCCCAGCTACTTTGGGAGGCTGAGGCAGGAGAATC 34876
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Qy      34877 GCTTGAACCCCAGAGGCGGATGTTGTAGTGAGCCAAGATCATGCCACTGGACTCCAGCCT 34936
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Db      34548 GCTTGAACCCCAGAGGCGGATGTTGTAGTGAGCCAAGATCATGCCACTGGACTCCAGCCT 34607

Qy      34937 GGGTGACAGAGTGAGACTCCATCCAAAAAAAAAGAAGAGCTGAGGTGATGGCCACCATCAG 34996
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Db      34608 GGGTGACAGAGTGAGACTCCATCCAAAAAAAAAGAAGAGCTGAGGTGATGGCCACCATCAG 34667

Qy      34997 CATCAGCCTGGAAGTTATAGCAGGATGCTAAGTTTCTCTAAAGCTGTCTTTCTTAGGACT 35056
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Db      34668 CATCAGCCTGGAAGTTATAGCAGGATGCTAAGTTTCTCTAAAGCTGTCTTTCTTAGGACT 34727

Qy      35057 TGAAAAAGATAACTTGGGTTTGTATCCCATCTCTGCCATTAGTAGTTTACTGGCTTTGGA 35116
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Db      34728 TGAAAAAGATAACTTGGGTTTGTATCCCATCTCTGCCATTAGTAGTTTACTGGCTTTGGA 34787

Qy      35117 TAAATTACTTAGCCTTACTGAACCAACTTTGGATTTTTATAGAGATACTGTAATGAAAGG 35176
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Db      34788 TAAATTACTTAGCCTTACTGAACCAACTTTGGATTTTTATAGAGATACTGTAATGAAAGG 34847

Qy      35177 AATAAGGTATCAGTCTTAGCAGAGCATCCAGAGTGTTCCTATTAAAACCTAAATCATATC 35236
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Db      34848 AATAAGGTATCAGTCTTAGCAGAGCATCCAGAGTGTTCCTATTAAAACCTAAATCATATC 34907

Qy      35237 CTGTCATTGCTGTGCCCCAAACCATTCAATGGCTTCCCAACTCAAAGTTAAAAACTCATC 35296
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Qy      35297 TTTCCAGTGGCCTGCAAGAGCCTATGCTATCCGGTGTCTGACCTCATCTGTTGTTCCTTT 35356
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Qy      35357 CTCCCTCCCTTTCTTGGCTCCAGACGCACTCTGGTCTCCTTGCTGTTCCTTGAATACACC 35416
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Db      35028 CTCCCTCCCTTTCTTGGCTCCAGACGCACTCTGGTCTCCTTGCTGTTCCTTGAATACACC 35087

Qy      35417 AGGCACACTCTCTTCGCCTGAAACACTTTACCCCAGATATCTTAGCTTACTCTCTGCCTC 35476
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Db      35088 AGGCACACTCTCTTCACCTGAAACACTTTACCCCAGATATCTTAGCTTACTCTCTGCCTC 35147

Qy      35477 CCTCAATTCATTGATGAAATGTCTCAGTGAAGTCTTCTCTCTCTCCTCTGTAAAAGTATA 35536
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Db      35148 CCTCAATTCATTGATGAAATGTCTCAGTGAAGTCTTCTCTCTCTCCTCTGTAAAAGTATA 35207

Qy      35537 CTCTCTGTTCCCCTTCTTTACTGTTCTAGCTACTATTGCTGTGTGTAACAAATCACTCCCCA 35596
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Db      35208 CTCTCTGTTCCCCTTCTTTACTGTTCTAGCTACTATTGCTGTGTGTAACAAATCACTCCCCA 35267

Qy      35597 AATTTAATGAGTGAAAACATCAGCCATCATCTTATTTCTCACGGTTTCTGAGGGTCAGGA 35656
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Db      35268 AATTTAATGAGTGAAAACATCAGCCATCATCTTATTTCTCACGGTTTCTGAGGGTCAGGA 35327

Qy      35657 ATTCTGGAAGGGCTCAGCTGGGAGGTTCTGGCTCTATAATCTCTTATGCAGTGAGAGTCA 35716
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Db      35328 ATTCTGGAAGGGCTCAGCTGGGAGGTTCTGGCTCTATAATCTCTTATGCAGTGAGAGTCA 35387

Qy      35717 GATGCTGGCTAAAACTGAAACAAAGCAGGGTTCTAGTAGCTGAGGGCTGGCTGGGTCTCT 35776
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Db      35388 GATGCTGGCTAAAACTGAAACAAAGCAGGGTTCTAGTAGCTGAGGGCTGGCTGGGTCTCT 35447

Qy      35777 CAGATATAGTTCAGATCTCCTCCAGGGGGTCTCTCCACGTGGGCTAGTCTGAACTTCCTC 35836
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Db      35448 CAGATATAGTTCAGATCTCCTCCAGGGGGTCTCTCCACGTGGGCTAGTCTGAACTTCCTC 35507

Qy      35837 ACAGCATGGTGGCCTCAGGGCAGTGGACTCTGCATAGTGGCTGAAGGCTTCGCAGCTGAG 35896
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Qy      35897 TATTCCAGCAAGCAAAGTGGGAGCTGTATTGCCTCATATGACCCAACCTTGGAATCCACA 35956
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Db      35568 TATTCCAGCAAGCAAAGTGGGAGCTGTATTGCCTCATATGACCCAACCTTGGAATCCACA 35627

Qy      35957 CAGCATCACTTCCGTGTATTCTACGGGTTGAAAAGTCACAAAAACCAACCAGTTTCAAGG 36016
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Qy      36017 AGAAGGAACAGAGATCACATTTCTCAATTGGAGAAGGGTCAAAGTCACATTGTAATCAGA 36076
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Qy      36077 GCCTATGGGATACGAAGTATTGCGGTCAGGTATGAAAAATTTGATTTGCTGCATCTGCTT 36136
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Qy      36137 TACTTTCTCCACAGCGTTCATGATCTGCTTCTCACATGATATTGACTTACGTCATTTCTG 36196
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Qy      36197 CGTTTCCTGTCTTCCACACTAAAATGTCAGCCTGTTTTGTTCACTGCTGTATCCCCAGAG 36256
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Qy      36257 CCTAGCACGGAGCCCAGCATGTAGTGGTATCCAATAAATACTTGTTGCATGAATGAATTC 36316
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Qy      36317 TGTCTTTTAATCCTAGCTATAGGTTTCTAAGTTAAATATTACTATAATCATCTTACAGAC 36376
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Qy      36377 GAGGGAAATGAGGCTCAAGAAGATTTGGTAACTTATGCGGGATCACTCAGCCACATAATG 36436
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Db      36048 GAGGGAAATGAGGCTCAAGAAGATTTGGTAACTTATGCGGGATCACTCAGCCACATAATG 36107

Qy      36437 GAAGAGACAGCATTGAAGTACACATGCTTGCTCTGTCTGCTCTTCCAAGCTGCTCATCAC 36496
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Qy      36497 ACAGCTGCACCTCTGAGGACTTCCCTCCCCAGTCCACCTCCACCCTTACCCAGAGACACA 36556
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Db      36168 ACAGCTGCACCTCTGAGGACTTCCCTCCCCAGTCCACCTCCACCCTTACCCAGAGACACA 36227

Qy      36557 CATGGCCACAATCCACTAGCAGACCAAAATTCAATTTTTCCCCAGTTGGTTGCACTCAAG 36616
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Db      36228 CATGGCCACAATCCACTAGCAGACCAAAATTCAATTTTTCCCCAGTTGGTTGCACTCAAG 36287

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Db      36288 CTGAGAGCAAAGCAATTGCACTTTAAATCCCCTTACAGCAGATATTTCAGAGCATGTTCG 36347

Qy      36677 GAAGAACCCATCACACTTGGCTTTTAGATCTTATTTCTGGTTTGTTACAAAAACACAATT 36736

Db      36348 GAAGAACCCATCACACTTGGCTTTTAGATCTTATTTCTGGTTTGTTACAAAAACACAATT 36407

Qy      36737 AAATGAAAGGTTAGGTAGCTTTTGAATGGCCAGCTCAAAGTTTTGGCTTATTTTTGCCTT 36796

Db      36408 AAATGAAAGGTTAGGTAGCTTTTGAATGGCCAGCTCAAAGTTTTGGCTTATTTTTGCCTT 36467

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Db      36468 GCTGTCTTTATAGGCATTTTACCAATATTTATCACTATTTCCCTTAGGGAACCCTTAGAT 36527

Qy      36857 CTGTGATATTTGAAATAATAAAGCCTCTCCATTGGCCCTTTAAAAGGTTTGTGGTAAAAC 36916

Db      36528 CTGTGATATTTGAAATAATAAAGCCTCTCCATTGGCCCTTTAAAAGGTTTGTGGTAAAAC 36587

Qy      36917 CACACCATTAACATTCACAGTTCCTTATTTATGAGGCCTGATTGCACTTATTTCCATATT 36976

Db      36588 CACACCATTAACATTCACAGTTCCTTATTTATGAGGCCTGATTGCACTTATTTCCATATT 36647

Qy      36977 TCTCACTGTTTCTCCGATGAGGATTTCACATAATAGTGTTTGAAGGCTAAAGACTTCAAA 37036

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Qy      37157 CAAAGTGACATTTAGTAATAGAGTCACATTCTCTAAGGCCTTTGCTTCTCCTTCTGA-TT 37215

Db      36828 CAAAGTGACATTTAGTAGTAGAGTCACATTCTCTAAGGCCTTTGCTTCTCCTTCTGAGTT 36887

Qy      37216 CTTATCATCTTTGAAGGTTATGTCATGGGCTGACTTCAAATCAACTTTTAAAATTATTAT 37275

Db      36888 CTTATCATCTTTGAAGGTTATGTCAT-GGCTGACTTCAAATC-ACTTTTAAAATTATTAT 36945

Qy      37276 GGCCTTCTTTAAATGTGAGTTCTGAAGGTGAGGGGCTTTATCTTTCTTTTGCTCCAGATT 37335

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Qy      37396 GACCTGGTTTTTCCCACTAGCTAACATCCTATTTTTATCTTTCCCCTTTGCACTAAAGGT 37455

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Qy      37696 CTATAATTTATACATCCTTGTACACAGGGCTTGCTGGGATATTGATGGAGAGAAGGAGGA 37755

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VERSION     AF222854.1  GI:9246844
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SOURCE      Homo sapiens (human)
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  AUTHORS   Barry,A.E., Bateman,M., Howman,E.V., Cancilla,M.R., Tainton,K.M.,
            Irvine,D.V., Saffery,R. and Choo,K.H.
  TITLE     The 10q25 neocentromere and its inactive progenitor have identical
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            modification
  JOURNAL   Genome Res. 10 (6), 832-838 (2000)
  MEDLINE   20314874
   PUBMED   10854414
REFERENCE   2  (bases 1 to 80202)
  AUTHORS   Barry,A.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JAN-2000) Chromosome Research Unit, The Murdoch
            Institute, 10th Floor, Royal Childrens Hospital, Flemington Rd.,
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ORIGIN

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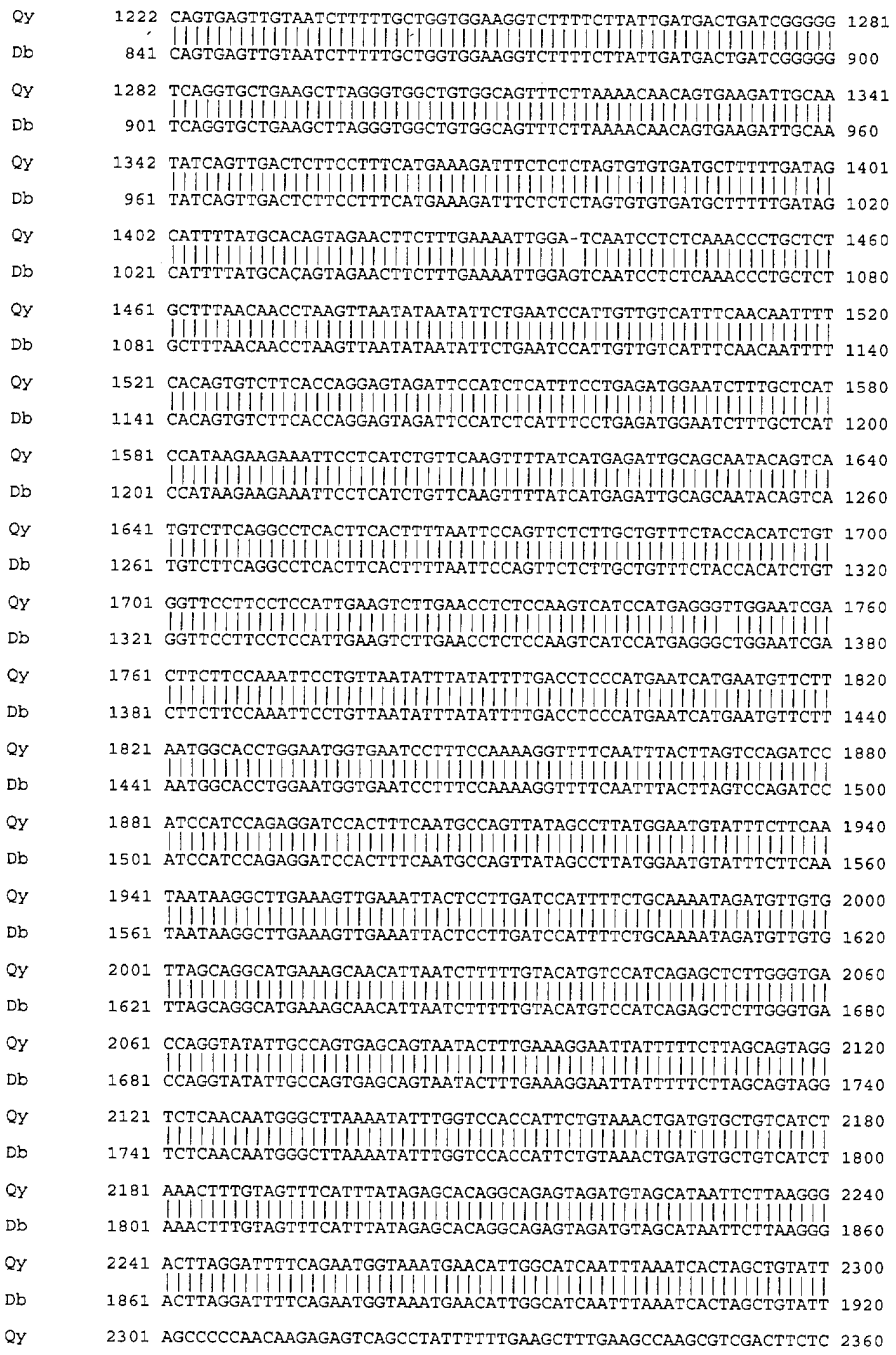
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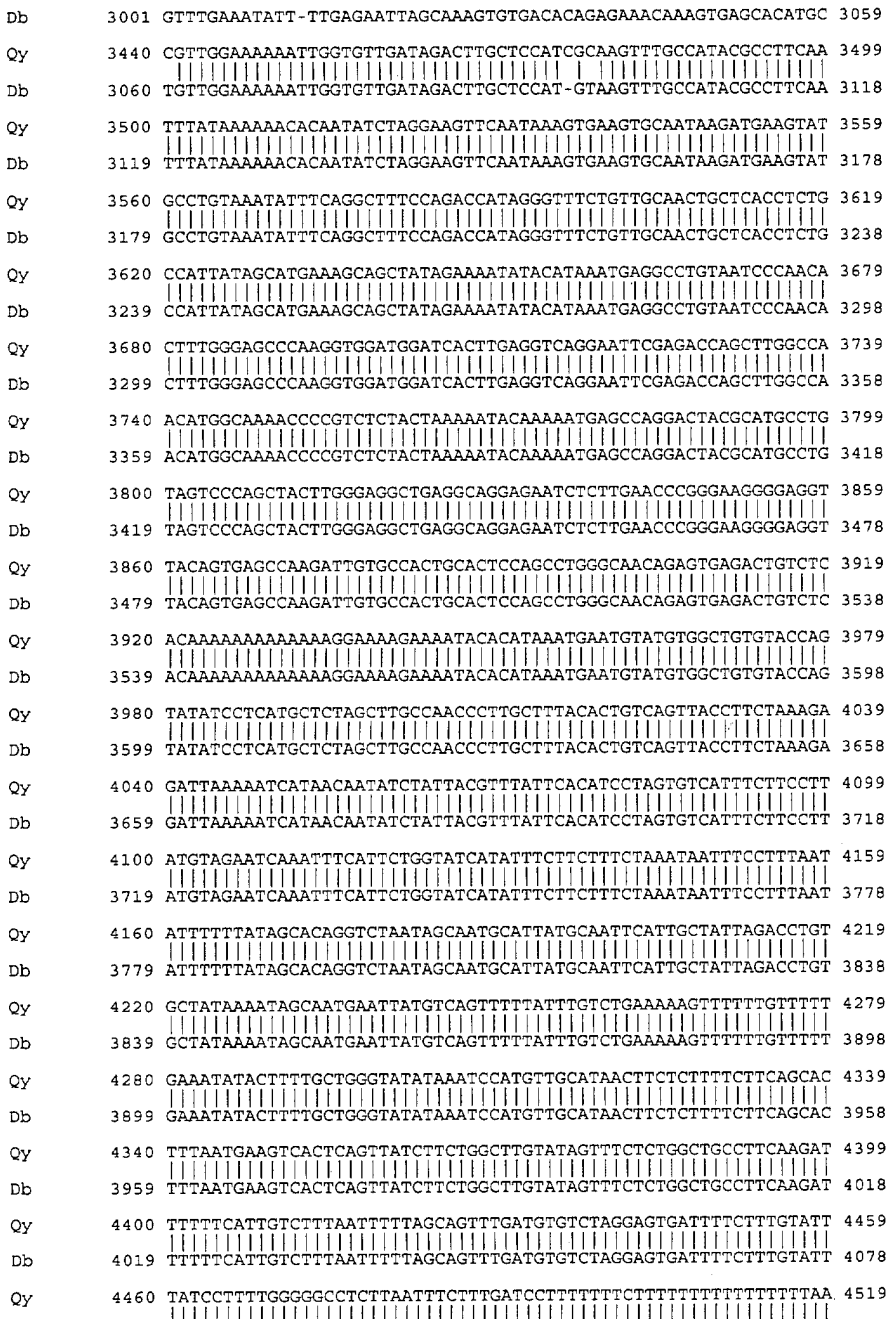
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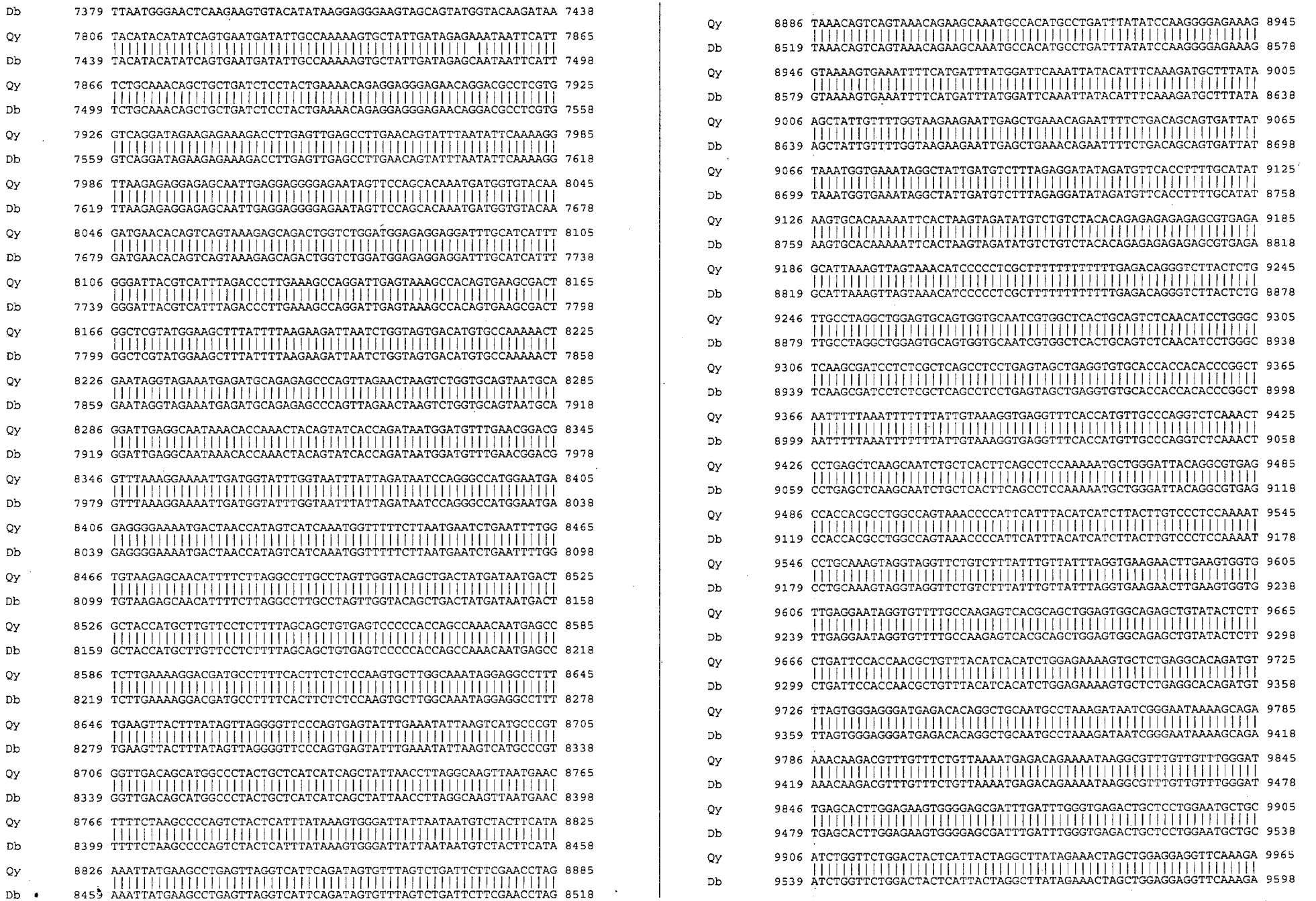
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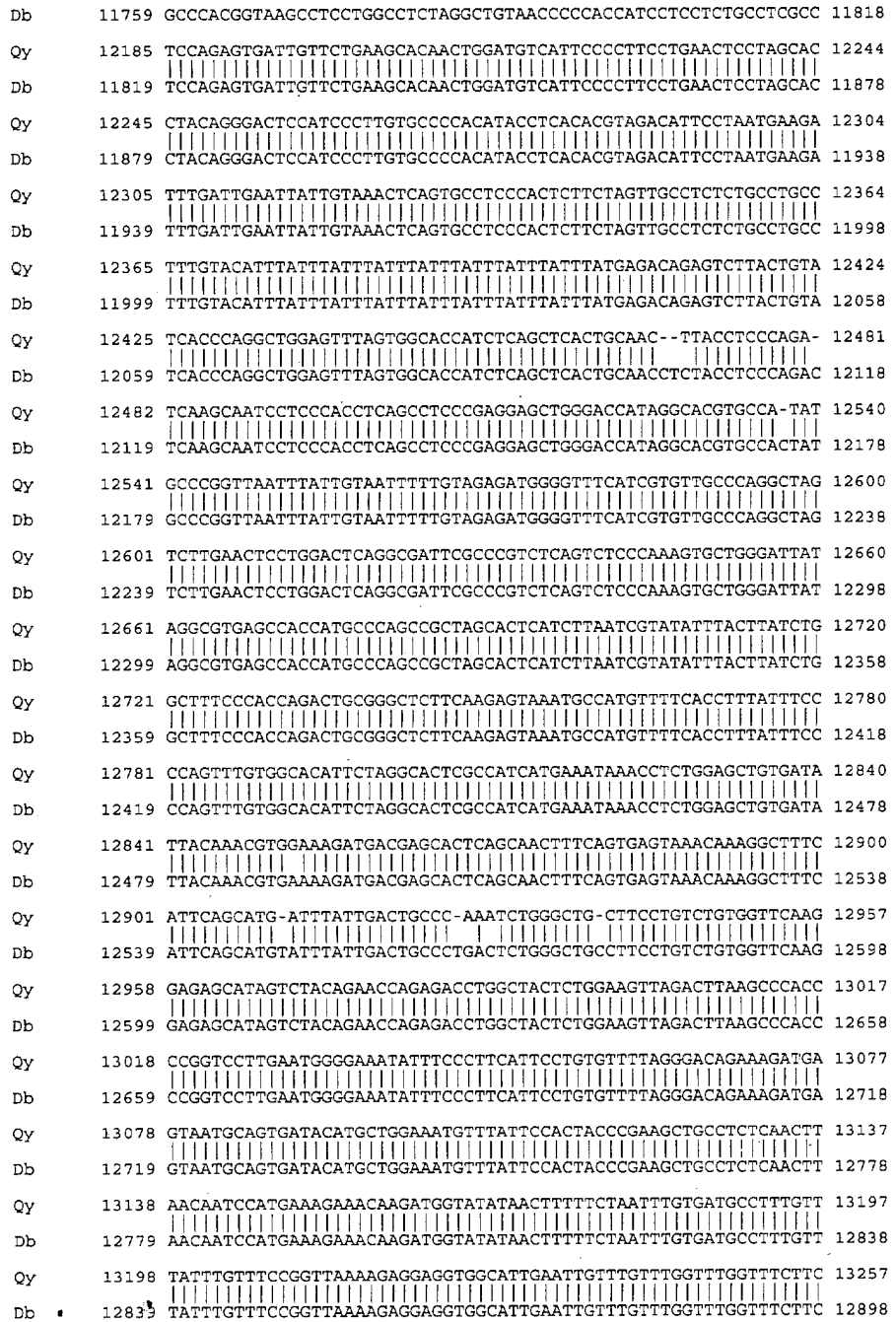
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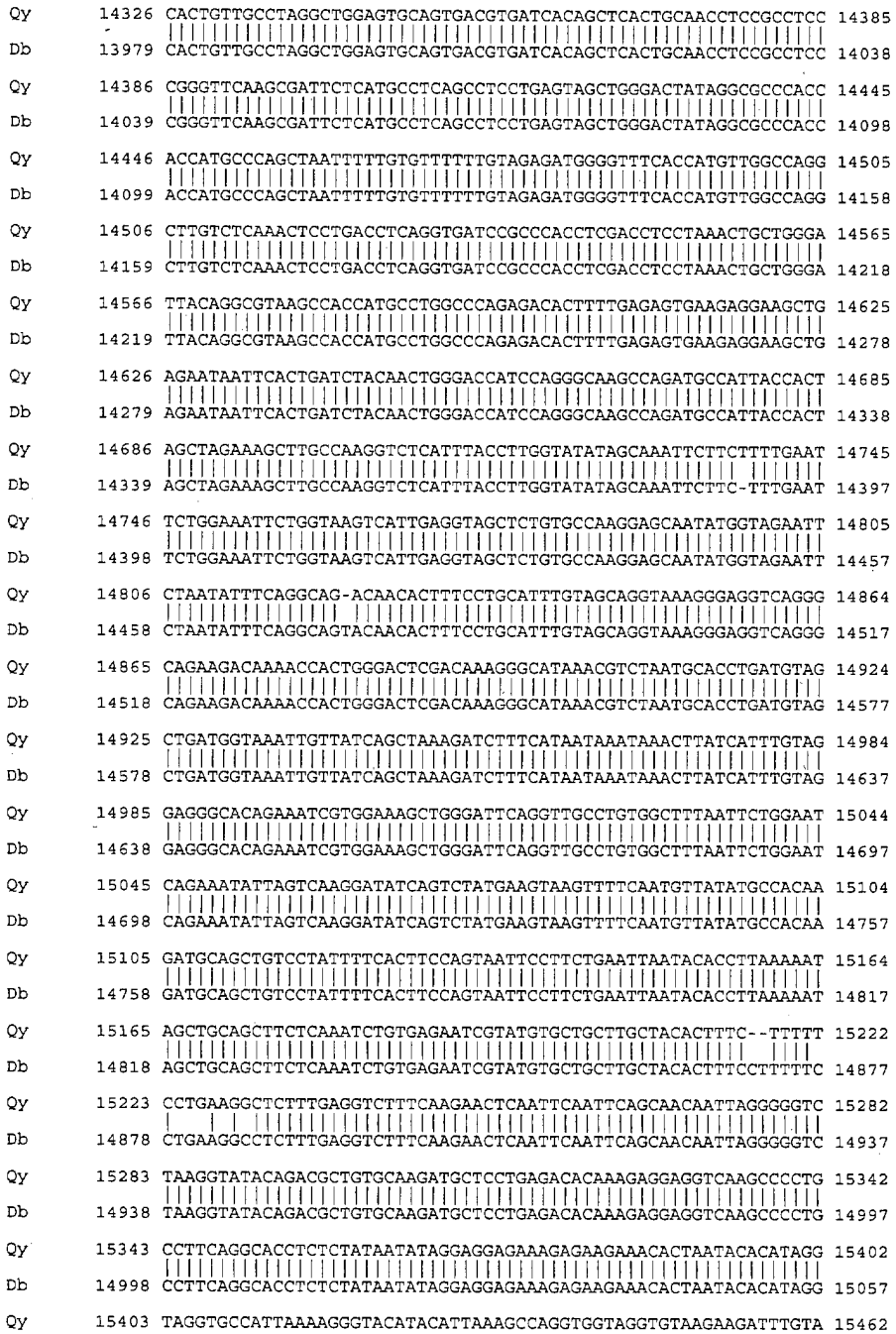
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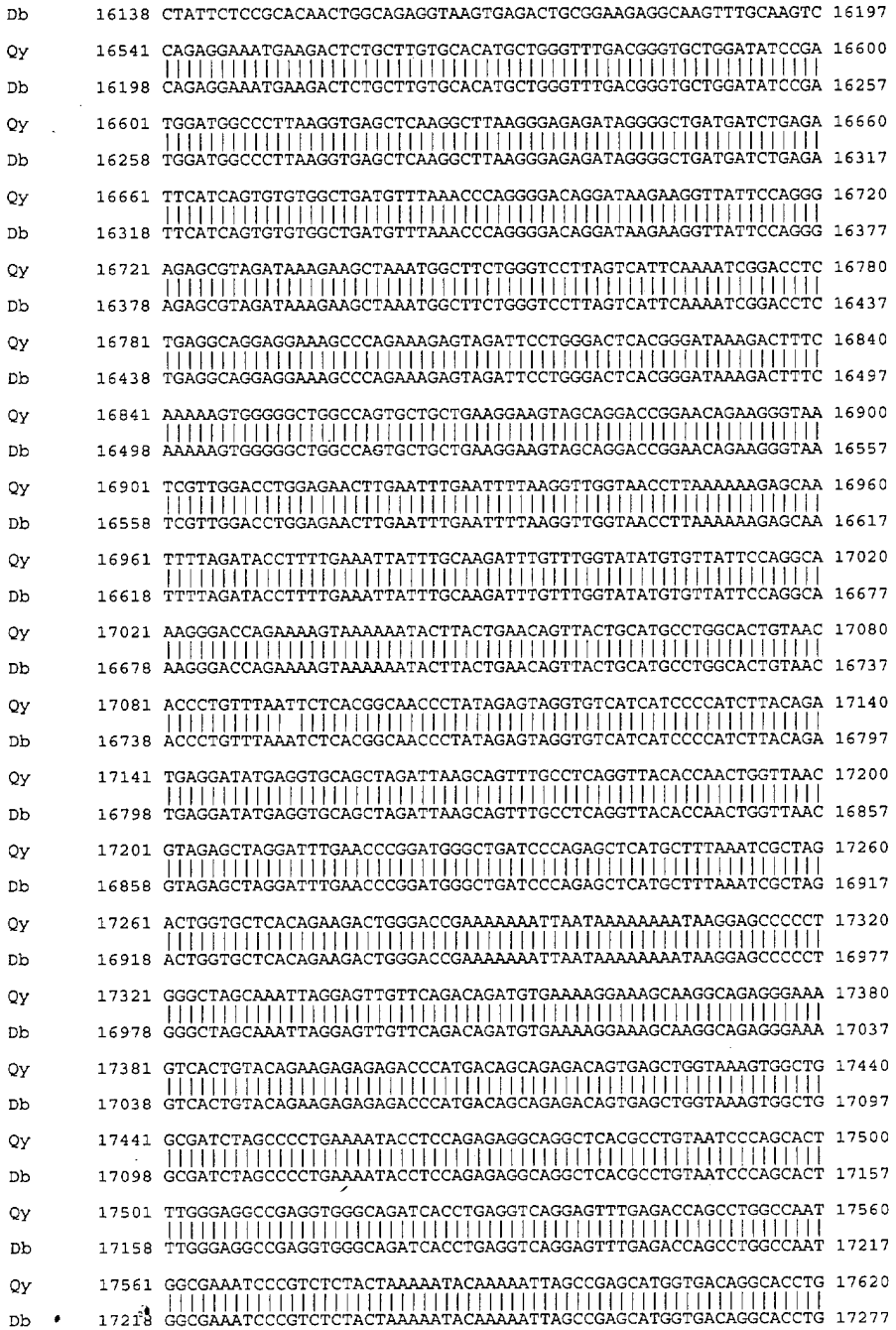
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Db 12659 CCGGTCCTTGAATGGGGAAATATTTCCCTTCATTCCTGTGTTTTAGGGACAGAAAGATGA 12718
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Db 12719 GTAATGCAGTGATACATGCTGGAAATGTTTATTCCACTACCCGAAGCTGCCTCTCAACTT 12778
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Db 13259 AAGCTGTATTCACACAAGCTCTCAAAGTGCCAGATTTTCATTGTGTTTTTAAACCATCTA 13318
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Db 13319 GGAAATGTTTGATTCTAATGAAACATTACTGCTGAAAATTGGGCTGAAATTGCTGGGCTG 13378
Qy 13738 GAAATATTGTTATAACTTCACATGATTCCAGTGTTGTATTATTATTTTTTCTTTTTCTTT 13797
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Qy      18760 TATCCCTTACAAGCGGAGTGTCAGCTGCCTCTTTTTGTCCACTGATTTAAGGCAAGATGA 18819
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Qy      18820 ACTGAAAGTGGCTATGATCACGTCTTCAAAAGCACACTCTGGCCCCTCGGCTGCAGGCGC 18879
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Qy      18880 CCTGCACATTCCCCAGCTGCGTGTCCGGTGGTGACACAGTGCATAATTGTGGCGCCTTCC 18939
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Qy      18940 TGGTGCAAACTGTCTCACTTAGCTCCGTCTTGCTGGCACAGCAGAAAGGAAGAAATCGAA 18999
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Qy      19000 AATGTTTGGATTTCAAAGGTAACAAGAAGCTGGAAAACAACTACTGGCCGAGTCTGAGAG 19059
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Qy      19060 TTTCAGCGGAGACTGGTGCAGCCTTGTGTTTTTCCACTGACAGCTGAAAATGAGCCCAGC 19119
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Qy      19120 TTCAGTGAAGCTTGTTTCCTTCCCTCCTCAAGGTTACCCACAATTCTCAGTTCTCTCAGG 19179
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Qy      19180 AAAGCCAAAAAAATGAATTTGAGGGTTTAGGATTGTGGTTCTTTTATCTATTACAGGATTG 19239
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Qy      19240 ATAATATGTTCCTCCACCAGATGTTCTGCTTGTAACAATACTCACTTCCTGACACTACTG 19299
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Qy      19300 CATATGCAGGAGTGTTACTACCAAGGTAAACACAGAATTGGCTGCCCAATTCCAAATCCC 19359
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Db      18958 CATATGCAGGAGTGTTACTACCAAGGTAAACACAGAATTGGCTGCCCAATTCCAAATCCC 19017

Qy      19360 TGAACTGAGTGAGAGAAATCAGAATTATAATAGGGGATTCAACAGAGCTGGCTACGGATG 19419
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Qy      19420 TGCCAGTGGTCAGATACTTTGCTCATCATACGCAGGTGCTGCTGCTCTAGCAACTGCTCA 19479
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Qy      19480 CTGCTTCATTTCCTGCCTTGGTCTTTAAATACTGCTTTTCTCAGCTCAATTGGCTTTCTT 19539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19138 CTGCTTCATTTCCTGCCTTGGTCTTTAAATACTGCTTTTCTCAGCTCAATTGGCTTTCTT 19197

Qy      19540 CCCTCTGGCAGTCACGTTTCTTTGGGTCAAACAGCAAATGATTCTTTAGAATCACCTGGT 19599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19198 CCCTCTGGCAGTCACGTTTCTTTGGGTCAAACAGCAAATGATTCTTTAGAATCACCTGGT 19257

Qy      19600 ACTCAAAGGAGCTACAAGACATTGGGCATCCACTTCCACTCTCTTGGAAAAACAATTTTA 19659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19258 ACTCAAAGGAGCTACAAGACATTGGGCATCCACTTCCACTCTCTTGGAAAAACAATTTTA 19317

Qy      19660 TGGAAGCCAAGGTTGCCATAGTGCCTCTTGAGGTTGTTTGCTCAGCCAAGGCCCAAGCTT 19719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19318 TGGAAGCCAAGGTTGCCATAGTGCCTCTTGAGGTTGTTTGCTCAGCCAAGGCCCAAGCTT 19377

Qy      19720 TGTGCTTCAAACATGAAATTAGAGAGCTTCAGAACAAGATCCACATTTTCAATGGCCTCA 19779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19378 TGTGCTTCAAACATGAAATTAGAGAGCTTCAGAACAAGATCCACATTTTCAATGGCCTCA 19437

Qy      19780 CCCAACTGGATAAAAGAACAATTGCCATATCTCAATGACCACCTTTT-TCAGGTGGGATG 19838
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db      19438 CCCAACTGGATAAAAGAACAATTGCCATATCTCAATGACCACCTTTTCTCAGGTGGGATG 19497

Qy      19839 GTAGATGCTGGAATGGGTCACAGCATTGCCCAACCAAACTTTGCAAAAAAGGCTGGAAGC 19898
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19498 GTAGATGCTGGAATGGGTCACAGCATTGCCCAACCAAACTTTGCAAAAAAGGCTGGAAGC 19557

Qy      19899 TCTGACTGGGGACCCTAAATATGCAAAAGTTGATAGGCTCTTCATGCAGAATATGAACCC 19958
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      19558 TCTGACTGGGGACCCTAAATATGCAAAAGTTAATAGGCTCTTCATGCAGAATATGAACCC 19617

Qy      19959 CGTGTATGGATATAGCTAAAGGGTTGGCCTTTATGTTTCTATTCCTTCACAAACCTGGTA 20018
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19618 CGTGTATGGATATAGCTAAAGGGTTGGCCTTTATGTTTCTATTCCTTCACAAACCTGGTA 19677

Qy      20019 GAATAGATATGCTTGTTTCCCTTTAAAAAATGTCAACAATTGCATTTATGATGCTGTGTA 20078
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19678 GAATAGATATGCTTGTTTCCCTTTAAAAAATGTCAACAATTGCATTTATGATGCTGTGTA 19737

Qy      20079 TAGTAACTCACAGATCATGCTCCATGAAAATGCTTCAGAACCCAATATAAGGAGATTTTT 20138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19738 TAGTAACTCACAGATCATGCTCCATGAAAATGCTTCAGAACCCAATATAAGGAGATTTTT 19797

Qy      20139 TAGCCATGTGTGACAAAAGAGAGGCCATTTCAGTGTTGAAATTGTTCAGAGAAGTATTTG 20198
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      19798 TAGCCATGTGTGACAAAAGAGAGGCCATTTCAGTGTTGAAATTCTTCAGAGAAGTATTTG 19857

Qy      20199 ATTATGTTTTCTCAGATCTTTTTATTTTTATTTTTTTTGAAACAGAGTCTCACTTTGTCA 20258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19858 ATTATGTTTTCTCAGATCTTTTTATTTTTATTTTTTTTGAAACAGAGTCTCACTTTGTCA 19917

Qy      20259 CCCAGGCTGGAGTACAGTGGCTGTGGTCTCGGCTCACTGCAACCTCTGCCTCCCAGGTTC 20318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19918 CCCAGGCTGGAGTACAGTGGCTGTGGTCTCGGCTCACTGCAACCTCTGCCTCCCAGGTTC 19977

Qy      20319 AAGCGATTCTCCTGTCAGCTTCCCGAATAGCTGGGATTACAGGCGCATGCACCACCATGC 20378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19978 AAGCGATTCTCCTGTCAGCTTCCCGAATAGCTGGGATTACAGGCGCATGCACCACCATGC 20037

Qy      20379 CTAATTTTTGTATTTTTAGTAGAGACAGAGTTTCGCCATGTTGACCAGGCTTGCCTTGAA 20438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20038 CTAATTTTTGTATTTTTAGTAGAGACAGAGTTTCGCCATGTTGACCAGGCTTGCCTTGAA 20097

Qy      20439 CTCCTGACTTCAGGTGATCCACCCACCTCAGCCTCCCAAAGCACTGGGATTACAGGCATG 20498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20098 CTCCTGACTTCAGGTGATCCACCCACCTCAGCCTCCCAAAGCACTGGGATTACAGGCATG 20157

Qy      20499 AGCCACCGTGCCCAGCCTGTTTTCTCAGATCCTGTA-TTTGTTTCTGAAGCCTTCATTTC 20557
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db      20158 AGCCACCGTGCCCAGCCTGTTTTCTCAGATCCTGTATTTTGTTTCTGAAGCCTTCATTTC 20217

Qy      20558 TATCTTCTTATTCATTTTGGAAGTAGTACACCTAAGTAAGGTTTTTAACAATCAAATATC 20617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20218 TATCTTCTTATTCATTTTGGAAGTAGTACACCTAAGTAAGGTTTTTAACAATCAAATATC 20277

Qy      20618 TTTGGAAAATTCCCTGGTTCCTTTCTTATTCCTACAAAAATATGTTCAGTATAGCTGATG 20677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20278 TTTGGAAAATTCCCTGGTTCCTTTCTTATTCCTACAAAAATATGTTCAGTATAGCTGATG 20337

Qy      20678 TTATGTTTCTTTCAAATTATTCATTTCTCTATCTCAGAATTTATCTCATGCCTAATTGTT 20737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20338 TTATGTTTCTTTCAAATTATTCATTTCTCTATCTCAGAATTTATCTCATGCCTAATTGTT 20397

Qy      20738 ATTGAATAGTCTTCACTTCTTGTCATCCAGTTTCTGGTCTCTTATTTCACTCTAAGTCTA 20797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20398 ATTGAATAGTCTTCACTTCTTGTCATCCAGTTTCTGGTCTCTTATTTCACTCTAAGTCTA 20457

Qy      20798 AGTGGCTATTAGAATAAAGAGCTTGTAACAGATTCTTTCTCCAATATGTCTTATCTTTTG 20857
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20458 ATTGGCTATTAGAATAAAGAGCTTGTAACAGATTCTTTCTCCAATATGTCTTATCTTTTG 20517

Qy      20858 ACTGCATGCCAGTGACAAACTGTTAACTGTTTTGATTCTTCATAACATTCCACAGAACAT 20917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      20518 ACTGCATGCCAGTGACAAACTGTTAACTGTTTTGATTCTTCATAACATTCCACAGAACAT 20577
Qy      20918 GCTGACTCCTCTCTTCCTGAAAGCAATGCCCAAGCACAGCATTGTTAGATAGTATGTACG 20977
Db      20578 GCTGACTCCTCTCTTCCTGAAAGCAATGCCCAAGCACAGCATTGTTAGATAGTATGTACG 20637
Qy      20978 CAACAGGGACATGGGTGCATAGCAAAAACTAGAAGGAAGGAGGACCTTCCTTAGCAATGG 21037
Db      20638 CAACAGGGACATGGGTGCATAGCAAAAACTAGAAGGAAGGAGGACCTTCCTTAGCAATGG 20697
Qy      21038 GTGATATGGTCCCTGGACTTAGACTCCAAAGGGTCGTGAGGTGAAACACACATCGTCCAT 21097
Db      20698 GTGATATGGTCCCTGGACTTAGACTCCAAAGGGTCGTGAGGTGAAACACACATCGTCCAT 20757
Qy      21098 ACCCAGGAAGCACACAGGTGGGATGGAAGAGCTGTGCCTAATGAAACTTCATCCACGTGG 21157
Db      20758 ACCCAGGAAGCACACAGGTGGGATGGAAGAGCTGTGCCTAATGAAACTTCATCCACGTGG 20817
Qy      21158 AGGTGGAGGAGGCTGCAGCTGCAAGAACTCAGAGCTGCCTTACCCAGACCAGGGACCAGG 21217
Db      20818 AGGTGGAGGAGGCTGCAGCTGCAAGAACTCAGAGCTGCCTTACCCAGACCAGGGACCAGG 20877
Qy      21218 GAGGGCTTTCTGGAGGAAACAGCCTCTGAACTGCCAGCTGATAGAGGAGCTCTACCTCAA 21277
Db      20878 GAGGGCTTTCTGGAGGAAACAGCCTCTGAACTGCCAGCTGATAGAGGAGCTCTACCTCAA 20937
Qy      21278 CTCTTCTGGTTCCCCAGGGCTGCTTTTCCACGTCCATTTATTGGCACTGAAGTTTGAATA 21337
Db      20938 CTCTTCTGGTTCCCCAGGGCTGCTTTTCCACGTCCATTTATTGGCACTGAAGTTTGAATA 20997
Qy      21338 CCTTCAGGGGCCCGAAAGCCTGCCAGGTCCTCTTCTCTGCAGAGCAATCACACCAACCTG 21397
Db      20998 CCTTCAGGGGCCCGAAAGCCTGCCAGGTCCTCTTCTCTGCAGAGCAATCACACCAACCTG 21057
Qy      21398 CAAAGGGCTAGGAAAGGGCTGTCATCATCTCCTACTCAGAAACTGGTTCACTGGAAGGAC 21457
Db      21058 CAAAGGGCTAGGAAAGGGCTGTCATCATCTCCTACTCAGAAACTGGTTCACTGGAAGGAC 21117
Qy      21458 TCAGGGGCCACTGAATACATCCTGGCAGCTTTCACAAGAAGGGCTTCTGACTCAAGGATG 21517
Db      21118 TCAGGGGCCACTGAATACATCCTGGCAGCTTTCACAAGAAGGGCTTCTGACTCAAGGATG 21177
Qy      21518 TTTCCATCTTTGCCAGGTCGCCTTTTCTCCTTCTCTTAGAGTTTGGAGGACGCAAATGTG 21577
Db      21178 TTTCCATCTTTGCCAGGTCGCCTTTTCTCCTTCTCTTAGAGTTTGGAGGACGCAAATGTG 21237
Qy      21578 CTGAGAAGTCAACCTTTCCTGCAAGGTGAGACACAAGGGCCTTTCCCAGCAGAAAGAAGA 21637
Db      21238 CTGAGAAGTCAACCTTTCCTGCAAGGTGAGACACAAGGGCCTTTCCCAGCAGAAAGAAGA 21297
Qy      21638 GAGCAAATGGAAGGTCCTTCTTCCTCCAGTAGAGGATGGACTCTGTCTGGCAGCCACCCA 21697
Db      21298 GAGCAAATGGAAGGTCCTTCTTCCTCCAGTAGAGGATGGACTCTGTCTGGCAGCCACCCA 21357
Qy      21698 ACAGGAAAAGCACAATGCATGCCTGCCTGCTTCCCTCCCTCCCTCCGTTTCTCCCTCCCT 21757
Db      21358 ACAGGAAAAGCACAATGCATGCCTGCCTGCTTCCCTCCCTCCCTCCGTTTCTCCCTCCCT 21417
Qy      21758 CCCTCCTTCCTCCCTTCCATTCTCTTCCCTTCCCCTCCCTTCCCTTCCCCTCCCTTCCCT 21817
Db      21418 CCCTCCTTCCTCCCTTCCATTCTCTTCCCTTCCCCTCCCTTCCCTTCCCCTCCCTTCCCT 21477
Qy      21818 TCCCCTCCCCTCCCCTTCCCTTCTCCCTCTCCTTCCCTTCCTCTTCCCTTCCTTCCTCTT 21877
Db      21478 TCCCCTCCCCTCCCCTTCCCTTCTCCCTCTCCTTCCCTTCCTCTTCCCTTCCTTCCTCTT 21537
Qy      21878 CCCTTCCTTTCCCCTCCCCTTCCTTTCCCTTCCTCCCTCCCTTCCTCCCTTCTTTCCTTC 21937
Db      21538 CCCTTCCTTTCCCCTCCCCTTCCTTTCCCTTCCTCCCTCCCTTCCTCCCTTCTTTCCTTC 21597
Qy      21938 CCTTCTTTCCTTCCTCATTTCCTCCCTTCCTTCCTTCCTTCCTTCCTTTCTTCCTACTTT 21997
Db      21598 CCTTCTTTCCTTCCTCATTTCCTCCCTTCCTTCCTTCCTTCCTTTCTTCCTACTTT 21657

Qy      21998 CCTACCTTTAGGGCTCTGTGTCTTTGGAGTCCATTCTGATTATGCTGTAATGTCTGCCCC 22057
Db      21658 CCTACCTTTAGGGCTCTGTGTCTTTGGAGTCCATTCTGATTATGCTGTAATGTCTGCCCC 21717
Qy      22058 TTCCTCTTCTCTGTCAAAAAATGAAAGACATGGAAGCCACTTGCCTTTTACTGAATTAAA 22117
Db      21718 TTCCTCTTCTCTGTCAAAAAATGAAAGACATGGAAGCCACTTGCCTTTTACTGAATTAAA 21777
Qy      22118 AATTAGTAAAAGAGCTAAAAATTAATGGTTAAAAATGTACGCATAAATTATGCAGTATAC 22177
Db      21778 AATTAGTAAAAGAGCTAAAAATTAATGGTTAAAAATGTACGCATAAATTATGCAGTATAC 21837
Qy      22178 TAACCAATGAAAAGATACACTTCTCTTAATTAAAAGCTGACAGGGAGGGAAACAAGAAAA 22237
Db      21838 TAACCAATGAAAAGATACACTTCTCTTAATTAAAAGCTGACAGGGAGGGAAACAAGAAAA 21897
Qy      22238 GAGAAACACAAAACAATAATCTAAATGACCTATTAGTTGGAAGAACAACATCAGAGAAAA 22297
Db      21898 GAGAAACACAAAACAATAATCTAAATGACCTATTAGTTGGAAGAACAACATCAGAGAAAA 21957
Qy      22298 TAGATACTGTGTATAGTCATGTGTATGTCTATGGAATAACATTTGTAGAGAAATCTGGAC 22357
Db      21958 TAGATACTGTGTATAGTCATGTGTATGTCTATGGAATAACATTTGTAGAGAAATCTGGAC 22017
Qy      22358 TGATCCTTTCTGAGTAAAGAGAGCTGTGGGTACAATTAAGGGGAGATTGAAAGGAATCCA 22417
Db      22018 TGATCCTTTCTGAGTAAAGAGAGCTGTGGGTACAATTAAGGGGAGATTGAAAGGAATCCA 22077
Qy      22418 AAAGCATAGCAGATGCTGTGCCTCACTGGAATGGTTGCCGATCTCCTCCAAACTATGAAG 22477
Db      22078 AAAGCATAGCAGATGCTGTGCCTCACTGGAATGGTTGCCGATCTCCTCCAAACTATGAAG 22137
Qy      22478 TGTTTGAGGCTCAACTTTAATATAATTAAGATACAAAGACAGAATGAGAGAAAGAGAGAA 22537
Db      22138 TGTTTGAGGCTCAACTTTAATATAATTAAGATACAAAGACAGAATGAGAGAAAGAGAGAA 22197
Qy      22538 GGGAGCTCACTGGAAGAACACTCAAGATTCCTTACTACTCATTCTCTAAAATTACAATTG 22597
Db      22198 GGGAGCTCACTGGAAGAACACTCAAGATTCCTTACTACTCATTCTCTAAAATTACAATTG 22257
Qy      22598 TTCTAGATGGAAAAGAAAAAAAGCTTCTCTGTTAAAAAAGGAGCTTGTGCTATAGGAGGT 22657
Db      22258 TTCTAGATGGAAAAGAAAAAAAGCTTCTCTGTTAAAAAAGGAGCTTGTGCTATAGGAGGT 22317
Qy      22658 TTAAAATATACTTCTGACCCATCTCCAACATTCTAAATCCTTCCCAGAAAAGTATGCCAA 22717
Db      22318 TTAAAATATACTTCTGACCCATCTCCAACATTCTAAATCCTTCCCAGAAAAGTATGCCAA 22377
Qy      22718 TCCCAAGAAATATTCAATCAAATTGCTGGAAAGAAAAATACAAAATATTAAAATGTATTA 22777
Db      22378 TCCCAAGAAATATTCAATCAAATTGCTGGAAAGAAAAATACAAAATATTAAAATGTATTA 22437
Qy      22778 GGAAGCGACAGTAATTAAATCAGAACTGGAGCAGGAATAGACCAGCAGATCAATGAGACA 22837
Db      22438 GGAAGCGACAGTAATTAAATCAGAACTGGAGCAGGAATAGACCAGCAGATCAATGAGACA 22497
Qy      22838 GACATCAAGTCCCGGAATGTGGACTTGCAAATGCATTAAGTAATATGATATGCAATAAAG 22897
Db      22498 GACATCAAGTCCCGGAATGTGGACTTGCAAATGCATTAAGTAATATGATATGCAATAAAG 22557
Qy      22898 GTGGCACAGTGAACCAATGGGAAAAAAATTAATCTTATAATAATTGATATTGCAATAATT 22957
Db      22558 GTGGCACAGTGAACCAATGGGAAAAAAATTAATCTTATAATAATTGATATTGCAATAATT 22617
Qy      22958 GTCTAGTAATTGGGGGAAGAAATAAGCTTATTCCTTATCTCATTTCTTTTTTTCTTTTTG 23017
Db      22618 GTCTAGTAATTGGGGGAAGAAATAAGCTTATTCCTTATCTCATTTCTTTTTTTCTTTTTG 22677
Qy      23018 AGACAGAGTCTCACTCTGGTAGCCCAGGCTGGAGTGCAGCGATGCGATCTCTGCCCACTG 23077
Db      22678 AGACAGAGTCTCACTCTGGTAGCCCAGGCTGGAGTGCAGCGATGCGATCTCTGCCCACTG 22737
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Qy      23078 CAACCTTGCTCTCCCGGGCTCAGGCGATTCTCCCACCTCAGCCTCCCGAGCAGCTGAACT 23137
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Db      22738 CAACCTTGCTCTCCCGGGCTCAGGCGATTCTCCCACCTCAGCCTCCCGAGCAGCTGAACT 22797

Qy      23138 ACAGGCGTGTGCCACCACTCCCGGCAATTTTTTTTTTCCATTTTTAGTAAAAATGGGGTTT 23197
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      22798 ACAGGCGTGTGCCACCACTCCCGGCAATTTTTTTTTTCCATTTTTAGTAGAAATGGGGTTT 22857

Qy      23198 CACCATGTTGCCTGGGCTGGTCTTGAACTCCTGGGCTCAGGCAATCCACCCGCCTTGGCC 23257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22858 CACCATGTTGCCTGGGCTGGTCTTGAACTCCTGGGCTCAGGCAATCCACCCGCCTTGGCC 22917

Qy      23258 TCCCAAAGTGCTAGCATTACAGGCATGAGCCACCGCGCCTGGCAGCTCATTTCTTAGACT 23317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22918 TCCCAAAGTGCTAGCATTACAGGCATGAGCCACCGCGCCTGGCAGCTCATTTCTTAGACT 22977

Qy      23318 AAATAAATTGGAGATGGCTAAAAGATTTCTATGTAGGCCAACTATGTTTTTAAAAAG-TT 23376
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      22978 AAATAAATTGGAGATGGCTAAAAGATTTCTATGTAGGCCAACTATGTTTTTAAAAAGTTT 23037

Qy      23377 TTTTTTTTAAGGATATCTGCTGGAACCAATCATGCCACCAACCAAAGATGCAAGACTATA 23436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23038 TTTTTTTTAAGGATATCTGCTGGAACCAATCATGCCACCAACCAAAGATGCAAGACTATA 23097

Qy      23437 AAACATACCCAGTTTTTCAAAGCATTTAAAAATTATTCTAAAAATATTTTTTCTCCAGAA 23496
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Db      23098 AAACATACCCAGTTTTTCAAAGCATTTAAAAATTATTCTAAAAATATTTTTTCTCCAGAA 23157

Qy      23497 ATTTTGCATTGATTCCCTGAAGAAGCATTAATATGGGACCTGACTTATAAAATGATGAAC 23556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23158 ATTTTGCATTGATTCCCTGAAGAAGCATTAATATGGGACCTGACTTATAAAATGATGAAC 23217

Qy      23557 TCAATCTCCCCACTCAAGGTAGGAGTCTCTCAGATTTAAAAAATAAGCATCCTAGTCCTC 23616
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Db      23218 TCAATCTCCCCACTCAAGGTAGGAGTCTCTCAGATTTAAAAAATAAGCATCCTAGTCCTC 23277

Qy      23617 TTGTCCCTGTAAAAGTTAACCCTTACACCTGAAACACCAGGAGACTGGCGGTTGTTTGCA 23676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23278 TTGTCCCTGTAAAAGTTAACCCTTACACCTGAAACACCAGGAGACTGGCGGTTGTTTGCA 23337

Qy      23677 TAGGGGTTACAATTAAAGTTGAGCTACCTCTGACATCTATTAACACCAAAATTAGTAAAC 23736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23338 TAGGGGTTACAATTAAAGTTGAGCTACCTCTGACATCTATTAACACCAAAATTAGTAAAC 23397

Qy      23737 TATGCATGTATGGAGACTTTTATGATTGAACTTGTTTATTGAGTCAAGAGATATAGTTTA 23796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23398 TATGCATGTATGGAGACTTTTATGATTGAACTTGTTTATTGAGTCAAGAGATATAGTTTA 23457

Qy      23797 CAATGAAAATTTGGGGCATATCAAAATGACCTTGGCTTAGCTTAGCATTTGCTGATGTTA 23856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23458 CAATGAAAATTTGGGGCATATCAAAATGACCTTGGCTTAGCTTAGCATTTGCTGATGTTA 23517

Qy      23857 ACTATTTTCTTCATTGGGCTGATTTTAGTTGCTTAGGAAAAATACAAACACACACACTTT 23916
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23518 ACTATTTTCTTCATTGGGCTGATTTTAGTTGCTTAGGAAAAATACAAACACACACACTTT 23577

Qy      23917 AAAATTATATTAAAATCCCGTCCTAAACCTCAGAGTCCAGAACCGCATCCTAACACTGGT 23976
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23578 AAAATTATATTAAAATCCCGTCCTAAACCTCAGAGTCCAGAACCGCATCCTAACACTGGT 23637

Qy      23977 CATGCATAATATGTTTAAATTTTTGTGCTTTAAAAACTACAAATAAGGAATGTATTAATA 24036
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23638 CATGCATAATATGTTTAAATTTTTGTGCTTTAAAAACTACAAATAAGGAATGTATTAATA 23697

Qy      24037 GTTCCACAATCAATGGTCAGTTAGCCGAGGGAAGATTAGCATAGTTAAAGACTTAAAATG 24096
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23698 GTTCCACAATCAATGGTCAGTTAGCCGAGGGAAGATTAGCATAGTTAAAGACTTAAAATG 23757

Qy      24097 GCTTTACAACATATATCAAAAGGACAAAATAAGGGGAACAGAGTCTAGAAATGAGGAAAC 24156
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Db      23758 GCTTAACAACATATATCAAAAGGACAAAATAAGGGGAACAGAGTCTAGAAATGAGGAAAC 23817

Qy      24157 TGGGACACAGGCAAAAAAAAAAAAATGAGAACTGGGACATGAATAACGCAAGGGATAAGAC 24216
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Db      23818 TGGGACACAGGCAAAAAAAAAAAAATGAGAACTGGGACATGAATAACGCAAGGGATAAGAC 23877

Qy      24217 TAATACACAAAACACCCCAAATAAATAGCCAGCATTTGCTGAGCTCTTACTGTGAGCCTG 24276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23878 TAATACACAAAACACCCCAAATAAATAGCCAGCATTTGCTGAGCTCTTACTGTGAGCCTG 23937

Qy      24277 TTCTAAGCACTTTACATATATTAACTCATTTCATCCTCAAGGAACCATCTGAGGCAGGCA 24336
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23938 TTCTAAGCACTTTACATATATTAACTCATTTCATCCTCAAGGAACCATCTGAGGCAGGCA 23997

Qy      24337 CTGTTATCATCTCCATTTTACAGATAAGGAATAGACCCAGAGAGGCTGAGCAACTGGGCC 24396
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      23998 CTGTTATCATCTCCATTTTACAGATAAGGAATAGACCCAGAGAGGCTGAGCAACTGGGCC 24057

Qy      24397 TATTCCACAGCTACTATGGTGGAGATGAGATTTAAATCTAATCATTGGCTCCAGAGCCCA 24456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24058 TATTCCACAGCTACTATGGTGGAGATGAGATTTAAATCTAATCATTGGCTCCAGAGCCCA 24117

Qy      24457 TGCACCCAATGGCTGCACTAAGTGAATGCATGCGCTATCAACGTTGCCAAAAGTGGGCCA 24516
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24118 TGCACCCAATGGCTGCACTAAGTGAATGCATGCGCTATCAACGTTGCCAAAAGTGGGCCA 24177

Qy      24517 CAGCTCGGATCTGCGTTTTCCAGTAGCCAAAGCAGAGAGTGTGATCAGACCTCACTTTAA 24576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24178 CAGCTCGGATCTGCGTTTTCCAGTAGCCAAAGCAGAGAGTGTGATCAGACCTCACTTTAA 24237

Qy      24577 TAAGCAAGTCTCAAGCCAGAGAGAGGTGGTATCAGGCAGCAAACAGGCTGCTAGTCGAAA 24636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24238 TAAGCAAGTCTCAAGCCAGAGAGAGGTGGTATCAGGCAGCAAACAGGCTGCTAGTCGAAA 24297

Qy      24637 TCCCACTTCTTCTCTGAGTGGTCCATACAGTTTTACTCTACTTGCTTACAGAATGAAAAT 24696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24298 TCCCACTTCTTCTCTGAGTGGTCCATACAGTTTTACTCTACTTGCTTACAGAATGAAAAT 24357

Qy      24697 AGCTGGAGTTCAGGTGCGCTTTCAATGCCCTGTTGTCAGGATTGGGCTTTTCAAGTTTAT 24756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      24358 AGCTGGAGTTCAGGTGCGCTTTCAATGCCCTGTTGTCAGGATTGGGCTTTTCAAGTTTAT 24417

Qy      24757 TTTTTGTTGTTGTTTTTAATAGACTGTACTTTTTAGAAAATTTTTAGATTTACAGAAAGA 24816
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Db      24418 TTTTTGTTGTTGTTTTTAATAGACTGTACTTTTTAGAAAATTTTTAGATTTACAGAAAGA 24477

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Qy      24877 CTCTTACATTCATGCGGTACATTTGTTACAATTAATGAGCCAGGGCCGGCCGGGCACAGT 24936
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Qy      24937 GGTTCAGGCCCCTAATCCCAGCACTTTGGGAGGCAGAGGCAAGCGAATCACTTGAGGTCA 24996
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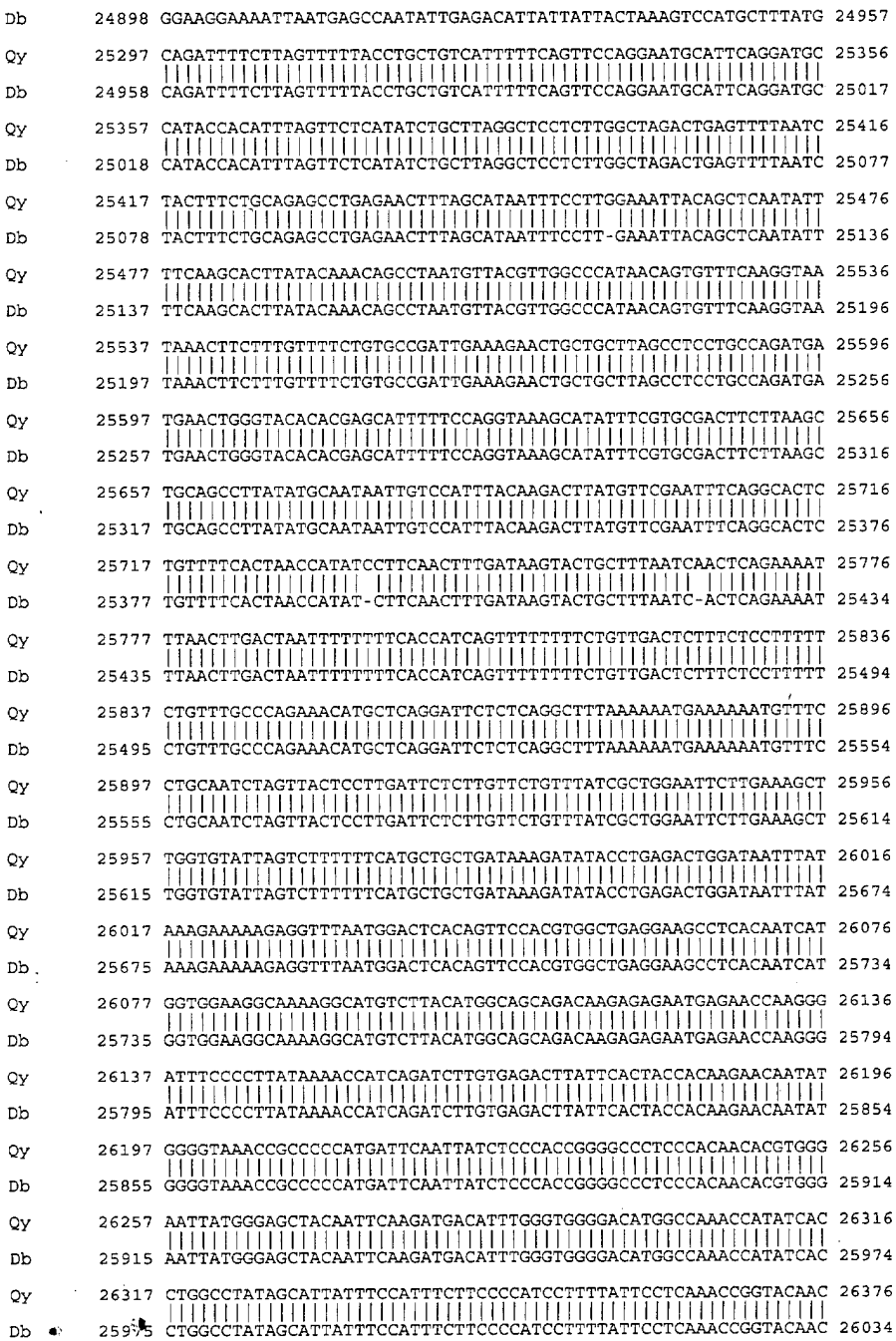
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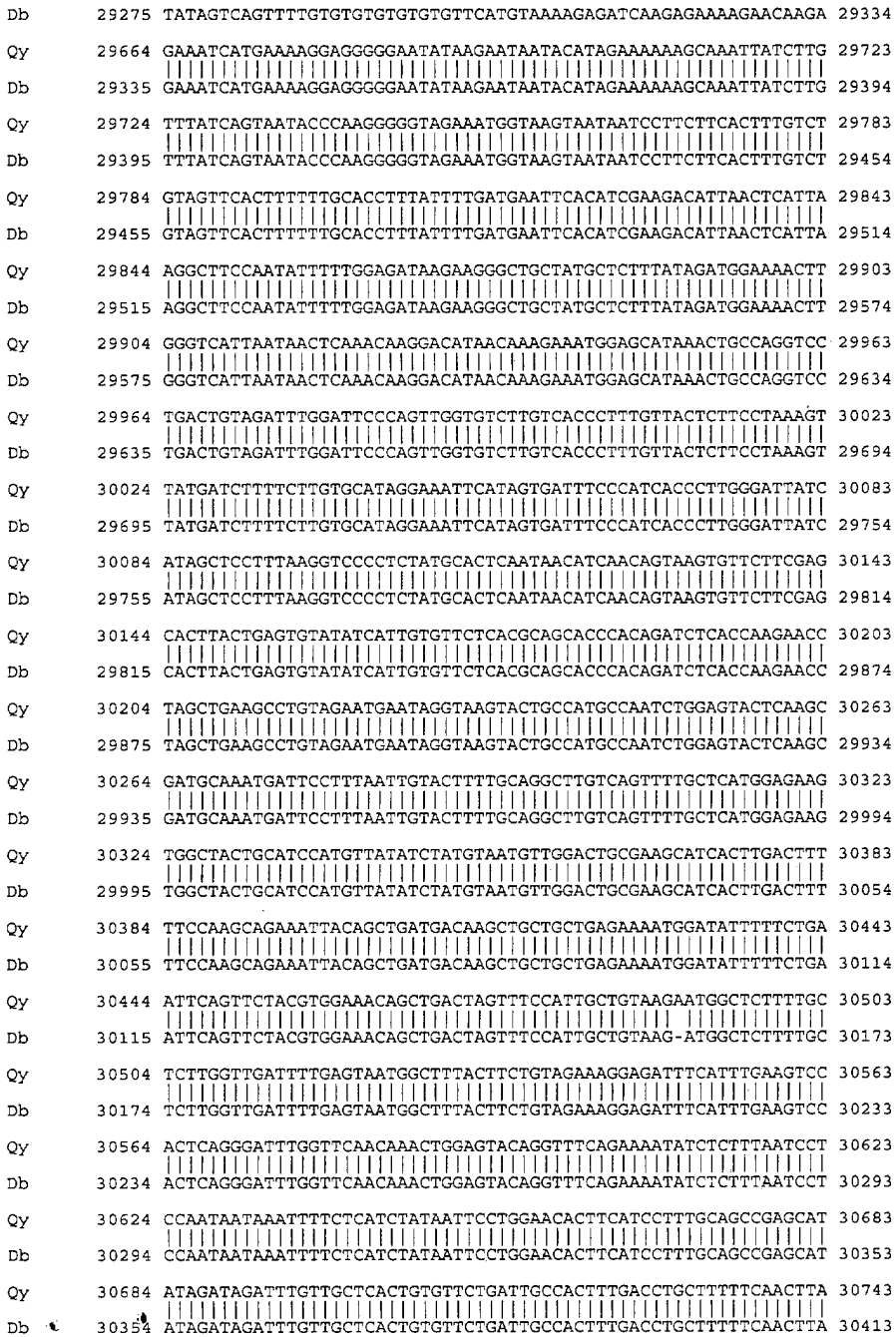
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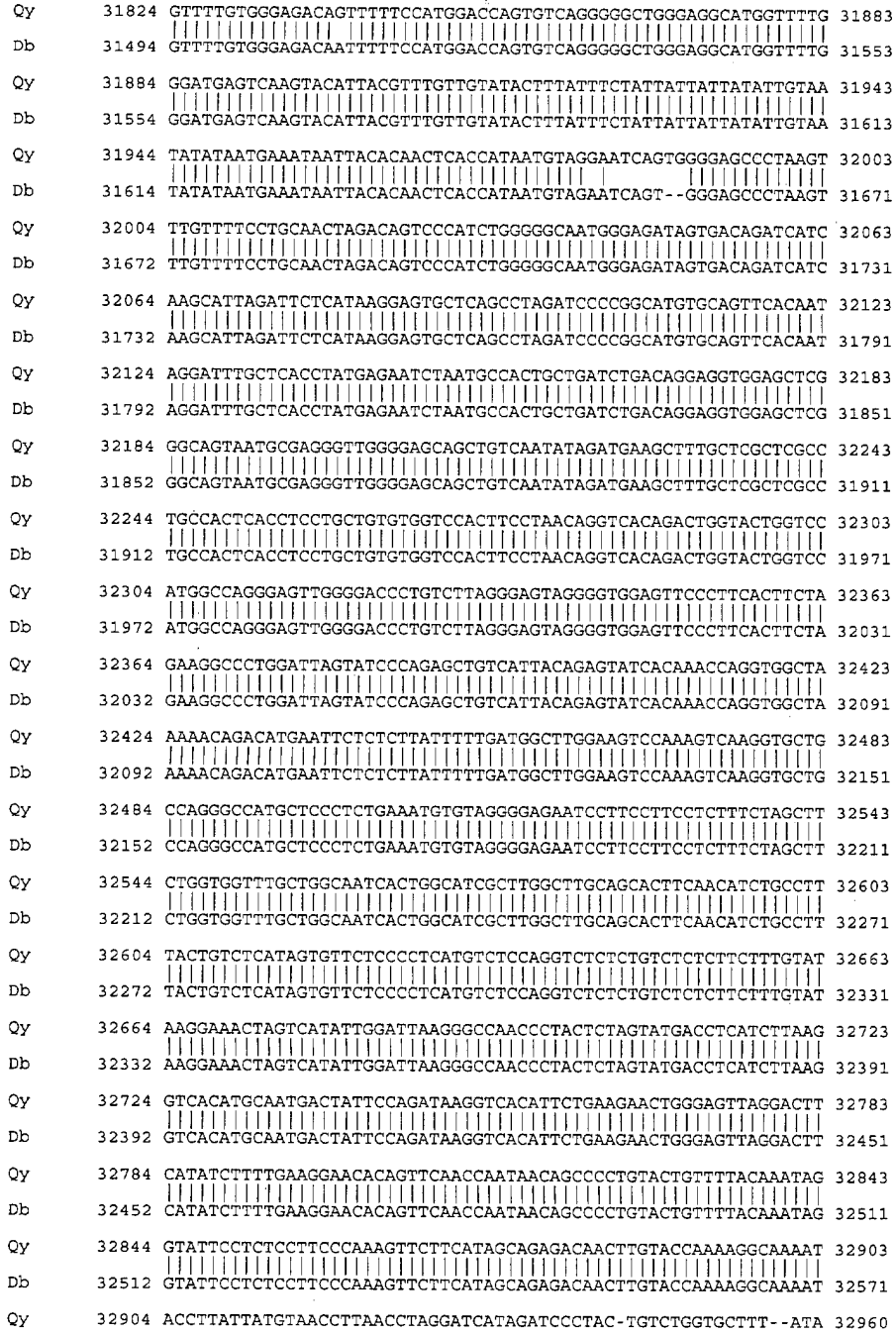
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Db 29935 GATGCAAATGATTCCTTTAATTGTACTTTTGCAGGCTTGTCAGTTTTGCTCATGGAGAAG 29994
Qy 30324 TGGCTACTGCATCCATGTTATATCTATGTAATGTTGGACTGCGAAGCATCACTTGACTTT 30383
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Db 31434 TACAGGGATTATTTAGAATCTTAGGGCAGTGGTGCCCAACCTTTTTGGCCCCAGGGACAG 31493


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Qy 33979 AACCCTCCAGGGAAAGGAGATGGGCTCCAGAGGCAGAAGAGGACGTTGAAGGGAATGGGG 34038

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Qy      34039 AGTGGGTGAAATATATAGACGATGGGGACCACCCAAGAGCAGTCGCTATTGCAAAACTGA 34098
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Qy      34099 GGAGAAGGAGAGTCTGGAGGGGGTGGTGGGAAGCTGGGTCTCCTAAGGAGGTTTTGACAA 34158
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Qy      34159 AAGCAGTCATGGAGCGGGCTTAGAAATCACAGTTGGGGACAGGGTAAAGTTCCTCGGGAT 34218
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Qy      34219 ATAGAGGATGAGATTAGAAGAGGTTCCAACTAGGGTAGTGTGGAGAAAAGCACTATTGAC 34278
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Qy      34279 CCAAAAAGGAAGGAGAATGTGGGTGGAAGTGGCAGAGAAAGAGGGGTTTGAGCAGAGAGT 34338
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Qy      34339 GGTGATTTTTCTAATGCAGAGTTGTGGGAGGTGGAGTGCAGGGAGCCAGGCTGGGTGGCT 34398
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Qy      34399 GTGCTGATGTGATTAAGCACTTACTGACTGCCAGGCAATGGGCTAAGTACCTGAGATGCT 34458
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Qy      34459 TTGTCTGTTATCCCTCCCGAAACCCCTCTGAGCAGGTGCAGTTATTATTCTCACTTCACA 34518
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Qy      34519 GATAAGGAAATTGAGGCACAGAGAA-TTGAGTAACTTACCCAAGGTGACATAGCTCATAT 34577
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Qy      34578 ATGGTAAAGCAGGCTTTGAACTCAGTCTAGCTCCCGAACCTAAGCTTGTAACTACTATGC 34637
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Qy      34638 TTTTCCCAAAAAAAGGGGGCTGGCACAAAAAGAGCTGA-GGGGGCTGGGCATGGTGGCTC 34696
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Db      34308 TTTTCCCAAAAAAAGGGGGCTGGCACAAAAAGAGCTGAGGGGGGCTGGGCATGGTGGCTC 34367
Qy      34697 ATGCCTGTAATCCCAGCACTTCGGGAGACTGAGGCAGGTGGTTCACCAGAGTTCAGGAGT 34756
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Qy      34757 TCGAGACCAGCCTGGTCAACATGGTGAAGCCCTGTCTCTACTAAAAATACAAAAATTAGC 34816
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Qy      34817 TGGGTGTGGTGGTGTGCACCTGTAGTCCCAGCTACTTTGGGAGGCTGAGGCAGGAGAATC 34876
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Qy      34877 GCTTGAACCCCAGAGGCGGATGTTGTAGTGAGCCAAGATCATGCCACTGGACTCCAGCCT 34936
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Qy      34937 GGGTGACAGAGTGAGACTCCATCCAAAAAAAAGAAGAGCTGAGGTGATGGCCACCATCAG 34996
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Qy      34997 CATCAGCCTGGAAGTTATAGCAGGATGCTAAGTTTCTCTAAAGCTGTCTTTCTTAGGACT 35056
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Qy      35057 TGAAAAAGATAACTTGGGTTTGTATCCCATCTCTGCCATTAGTAGTTTACTGGCTTTGGA 35116
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Qy      35117 TAAATTACTTAGCCTTACTGAACCAACTTTGGATTTTTATAGAGATACTGTAATGAAAGG 35176
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Qy      35177 AATAAGGTATCAGTCTTAGCAGAGCATCCAGAGTGTTCCTATTAAAACCTAAATCATATC 35236
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Qy      35237 CTGTCATTGCTGTGCCCCAAACCATTCAATGGCTTCCCAACTCAAAGTTAAAAACTCATC 35296
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Qy      35297 TTTCCAGTGGCCTGCAAGAGCCTATGCTATCCGGTGTCTGACCTCATCTGTTGTTCCTTT 35356
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Qy      35357 CTCCCTCCCTTTCTTGGCTCCAGACGCACTCTGGTCTCCTTGCTGTTCCTTGAATACACC 35416
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Db      35028 CTCCCTCCCTTTCTTGGCTCCAGACGCACTCTGGTCTCCTTGCTGTTCCTTGAATACACC 35087
Qy      35417 AGGCACACTCTCTTCGCCTGAAACACTTTACCCCAGATATCTTAGCTTACTCTCTGCCTC 35476
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Qy      35477 CCTCAATTCATTGATGAAATGTCTCAGTGAAGTCTTCTCTCTCTCCTCTGTAAAAGTATA 35536
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Qy      35537 CTCTCTGTTCCCCTTCTTTACTGTTCTAGCTACTATTGCTGTGTAACAAATCACTCCCCA 35596
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Db      35208 CTCTCTGTTCCCCTTCTTTACTGTTCTAGCTACTATTGCTGTGTAACAAATCACTCCCCA 35267
Qy      35597 AATTTAATGAGTGAAAACATCAGCCATCATCTTATTTCTCACGGTTTCTGAGGGTCAGGA 35656
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Db      35268 AATTTAATGAGTGAAAACATCAGCCATCATCTTATTTCTCACGGTTTCTGAGGGTCAGGA 35327
Qy      35657 ATTCTGGAAGGGCTCAGCTGGGAGGTTCTGGCTCTATAATCTCTTATGCAGTGAGAGTCA 35716
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Qy      35717 GATGCTGGCTAAAACTGAAACAAAGCAGGGTTCTAGTAGCTGAGGGCTGGCTGGGTCTCT 35776
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Qy      35777 CAGATATAGTTCAGATCTCCTCCAGGGGGTCTCTCCACGTGGGCTAGTCTGAACTTCCTC 35836
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Qy      36137 TACTTTCTCCACAGCGTTCATGATCTGCTTCTCACATGATATTGACTTACGTCATTTCTG 36196
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Qy 36197 CGTTTCCTGTCTTCCACACTAAAATGTCAGCCTGTTTTGTTCACTGCTGTATCCCCAGAG 36256
Db 35868 CATTTCCTGTCTTCCACACTAAAATGTCAGCCTGTTTTGTTCACTGCTGTATCCCCAGAG 35927
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Qy 38236 ATCAGTATTTTTTACAAATAGCTACTAAGAGCTACTAGAAAACCTGGGAATTCTTAAAAC 38295
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Qy 38296 CTTACCATGCTACTTGCTCTAAAATATTTTATTTTATGTTATTTTGTACATTTCTTTACC 38355
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Qy      38476 AGAATGTAAAACGAGGGCGAACAGATTTTTGACAGGAAGTATTCAGAGGTAGAAGGAAAT 38535
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Qy      39496 TGAAACCCTGTCTCTACTAAAAACGCAAAAATTAGCCAGGTGTGGTGGCATGCACCTGTA 39555
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RESULT 6
AX033912
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DEFINITION  Sequence 4 from Patent WO9851790.
ACCESSION   AX033912
VERSION     AX033912.1  GI:10280480
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Cancilla,M.R., Choo,K.H. and Du,S.D.
  TITLE     A novel nucleic acid molecule
  JOURNAL   Patent: WO 9851790-A 4 19-NOV-1998;
            CANCILLA MICHAEL ROBERT (AU) ; CHOO KONG HONG ANDY (AU) ; SART
            DESIREE DU (AU) ; AMRAD OPERATIONS PTY LTD (AU)
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ORIGIN

  Query Match           97.0%;  Score 38782.8;  DB 6;  Length 41008;
  Best Local Similarity  99.3%;  Pred. No. 0;
  Matches 39506;  Conservative    2;  Mismatches  166;  Indels   96;  Gaps   53;

Qy        292 GATTGATCTGTCATTATGAATGTCTGTATTCATTCCCTGATAGTATTTCTTTTTCTAAAT 351
              | ||||| |||   || | | || || | ||| |||| ||  | |||| ||||| |||
Db          2 GGTTGATTTGTNNATAAGGAAGTTTGGAATCAATCCCGGAAGGAATTTTTTTTTTAAAAA 61

Qy        352 ATTTTTCTGAATGTGTCTGCTATTAACATAGCCACTCTGGCTTTTTAAAATTAGTATTTT 411
              ||||||  ||| | || || ||:||| | |:||| | ||| |||||||||| ||| | |||
Db         62 ATTTTTTGGAAGG-GTTTGGTAWTAAAAAARCCAATTTGGGTTTTTAAAAATAGGAATTT 120
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Qy       412 TATGGTATATATTTTTCCTTTTTTTTTTTTTTTAAGTTTTAGATGTTATGTTTCCTTATAC 471
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Qy       472 TTAAAGTGGGTGTCTTATAGGCAGCATATATCTGGGTCTTGATGTATTATTTAATCTGAT 531
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Qy       532 AATCTCAACCTTTTTGTTGGAGTGTTTAGGCCATTTACATTTAGTGTAATTATAGACATG 591
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Qy      1610 GTTTTATCATGAGATTGCAGCAATACAGTCATGTCTTCAGGCCTCACTTCACTTTTAATT 1669
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Qy      1670 CCAGTTCTCTTGCTGTTTCTACCACATCTGTGGTTCCTTCCTCCATTGAAGTCTTGAACC 1729
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Qy      1730 TCTCCAAGTCATCCATGAGGGTTGGAATCGACTTCTTCCAAATTCCTGTTAATATTTATA 1789
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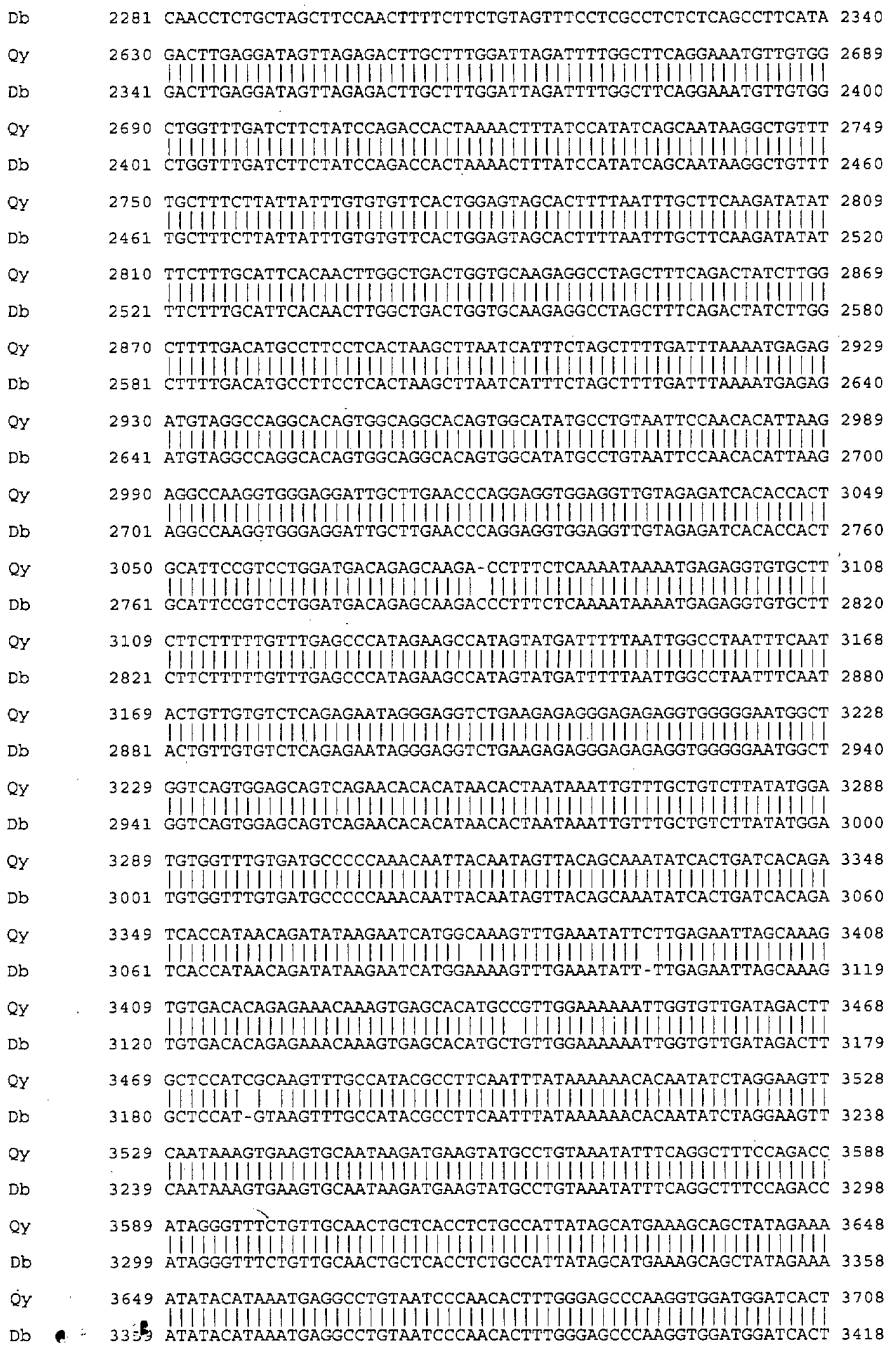
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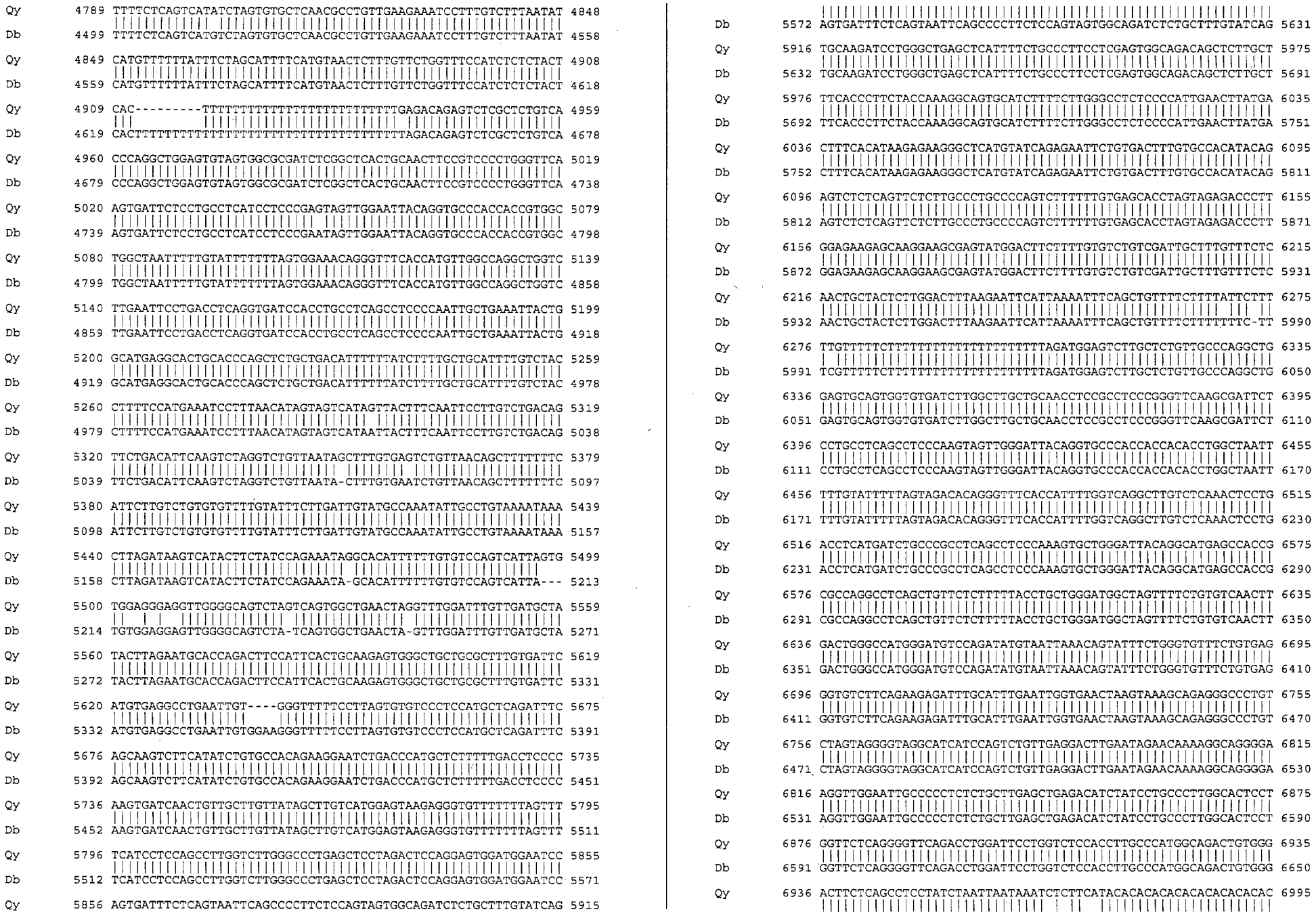
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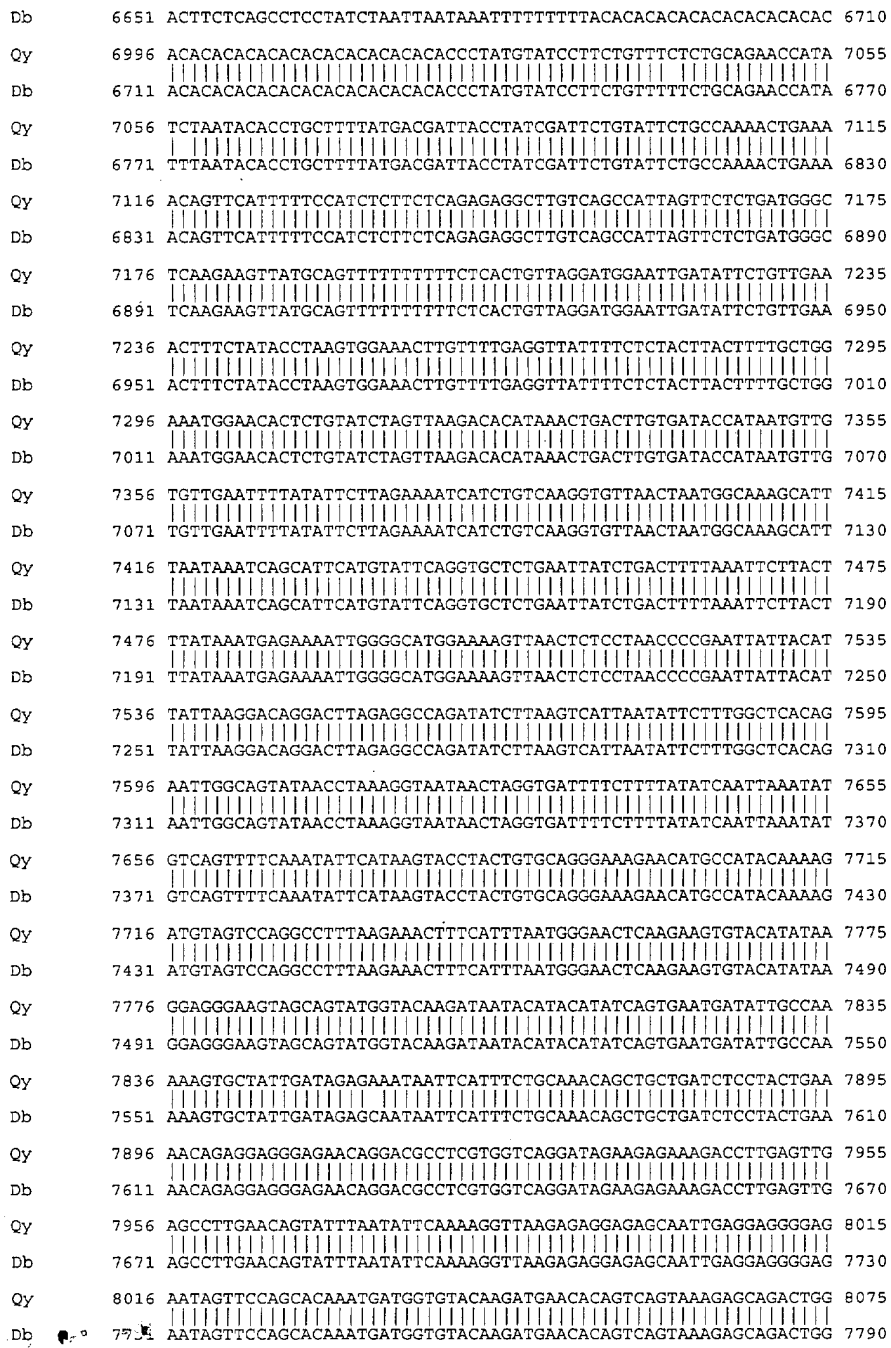
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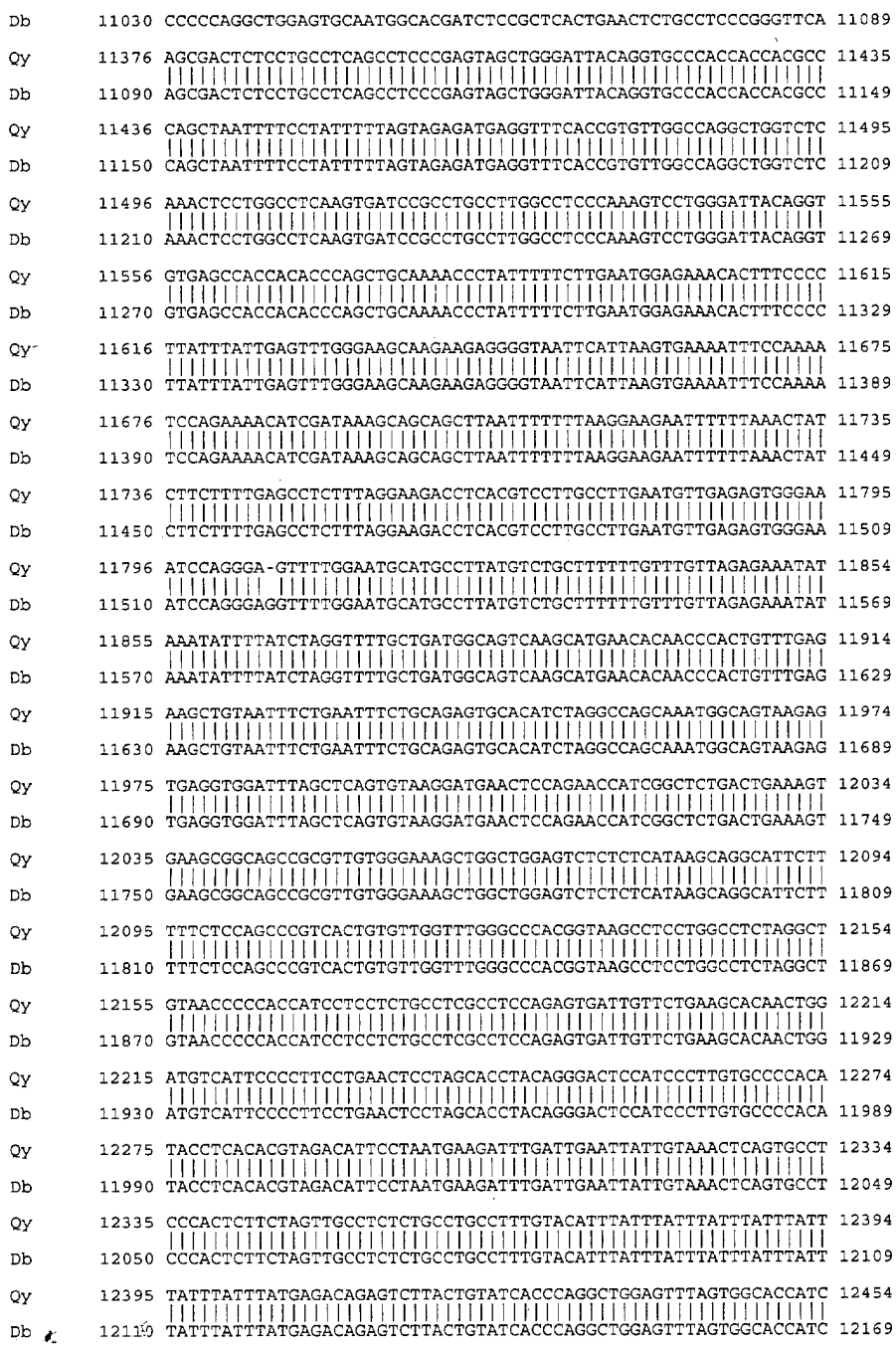
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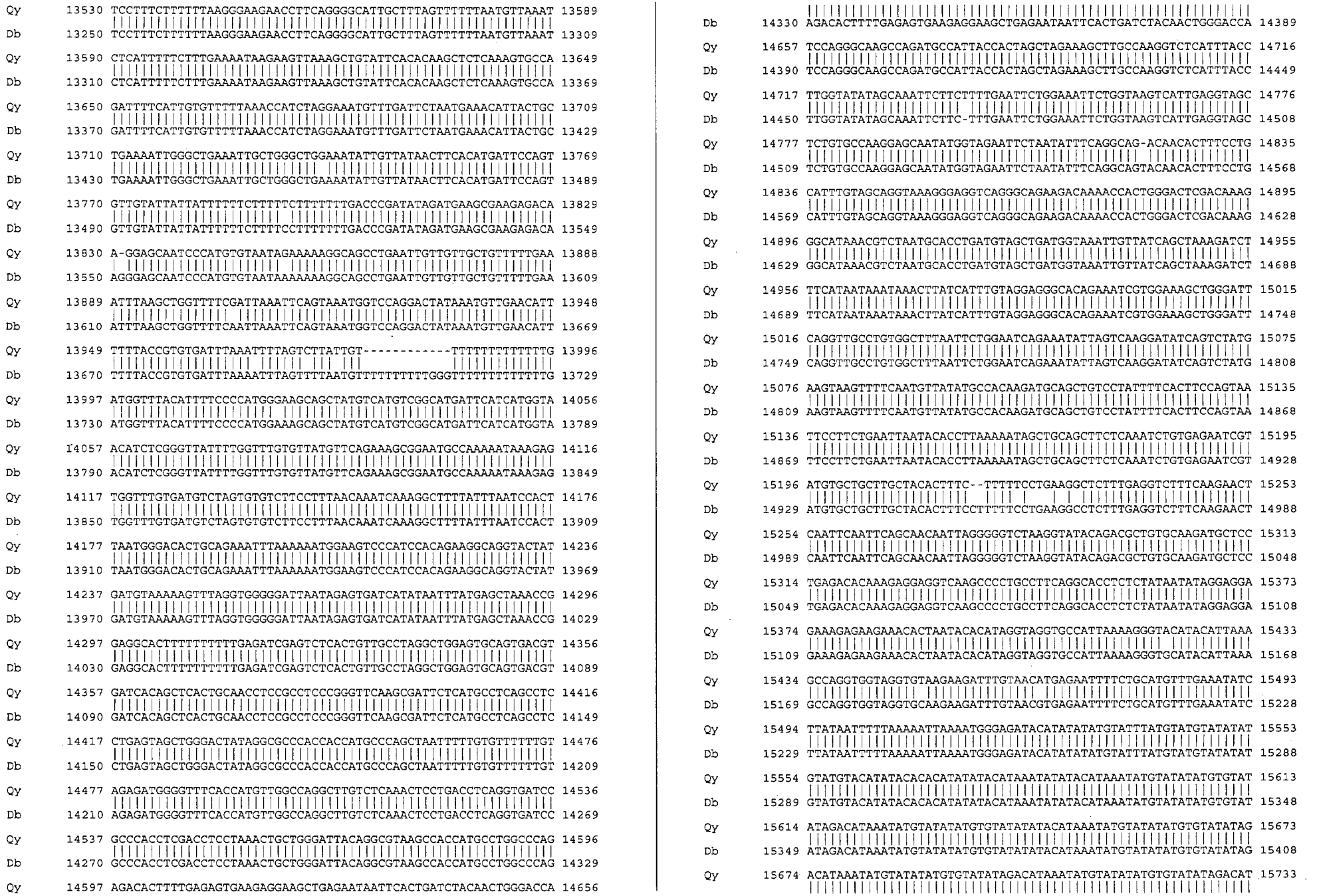
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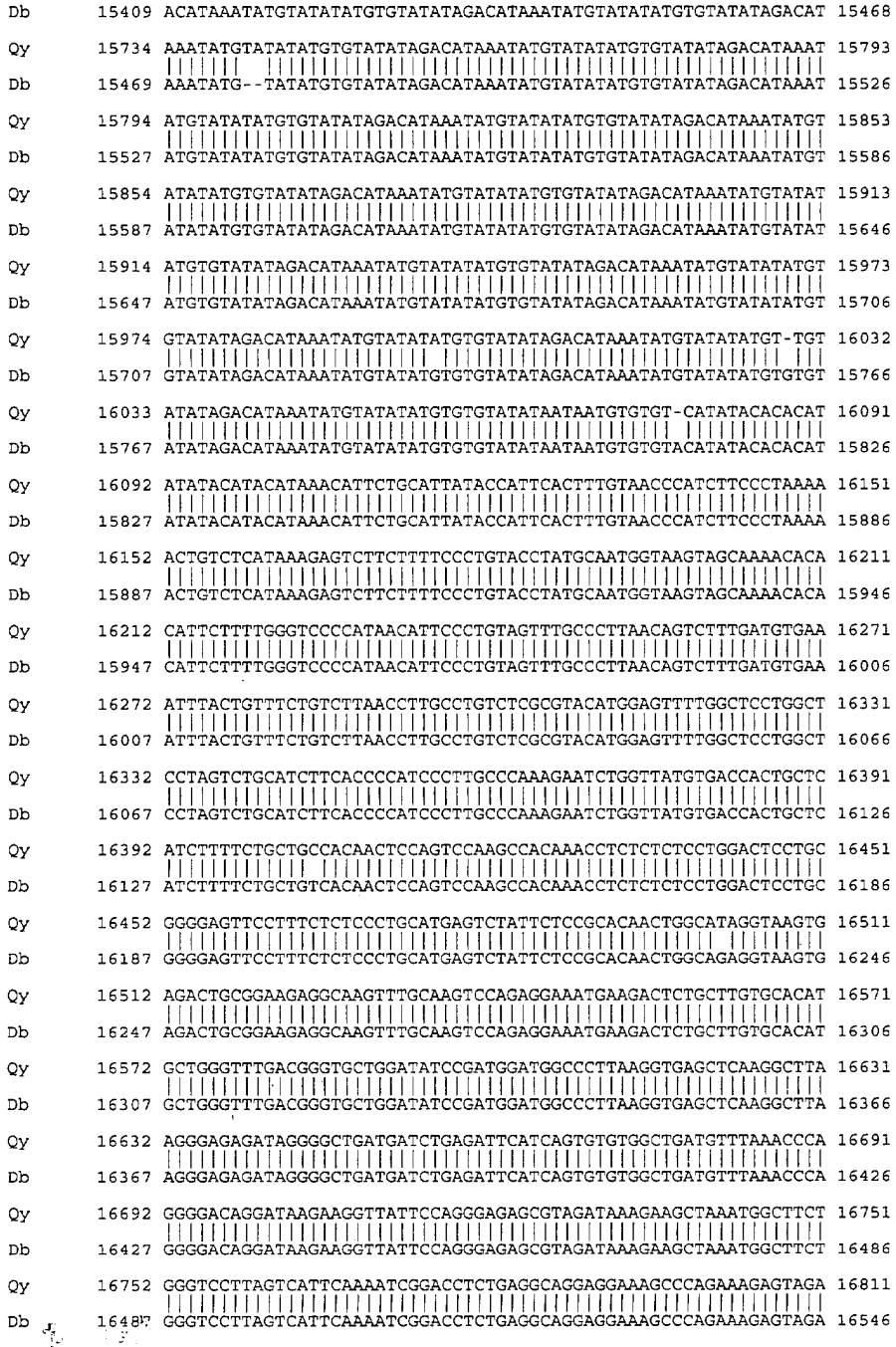
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Qy      18311 GAGTGGGGGTAAGTCCGTAAGCTGTAATGGAACCTAAACAAATACATGAAACGAGTAGGA 18370
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Qy      18611 GTATAAAAAAAAGGCACGGTGCTCCCTGGGTAGCCTTTCTGGACTTCAGAGCTAAATTGCA 18670
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Qy      18671 AAGTCAGTTTTACACATGTGATTTCATCTATGAAATTAGGGCAAGGTAGAAAACTGGCAC 18730
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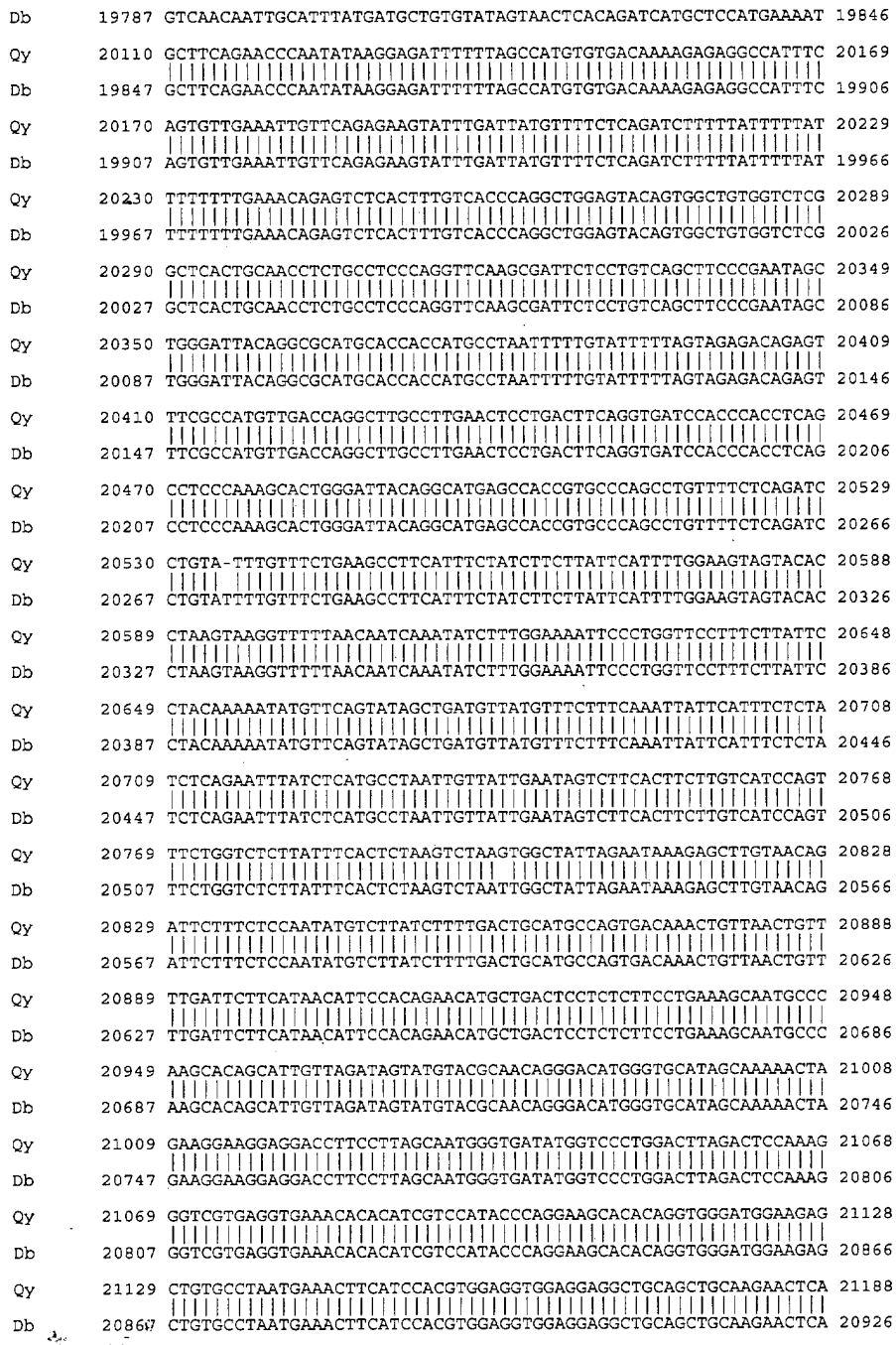
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Qy      19870 AACCAAACTTTGCAAAAAAGGCTGGAAGCTCTGACTGGGGACCCTAAATATGCAAAAGTT 19929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19607 AACCAAACTTTGCAAAAAAGGCTGGAAGCTCTGACTGGGGACCCTAAATATGCAAAAGTT 19666

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Db 19907 AGTGTTGAAATTGTTCAGAGAAGTATTTGATTATGTTTTCTCAGATCTTTTTATTTTTAT 19966
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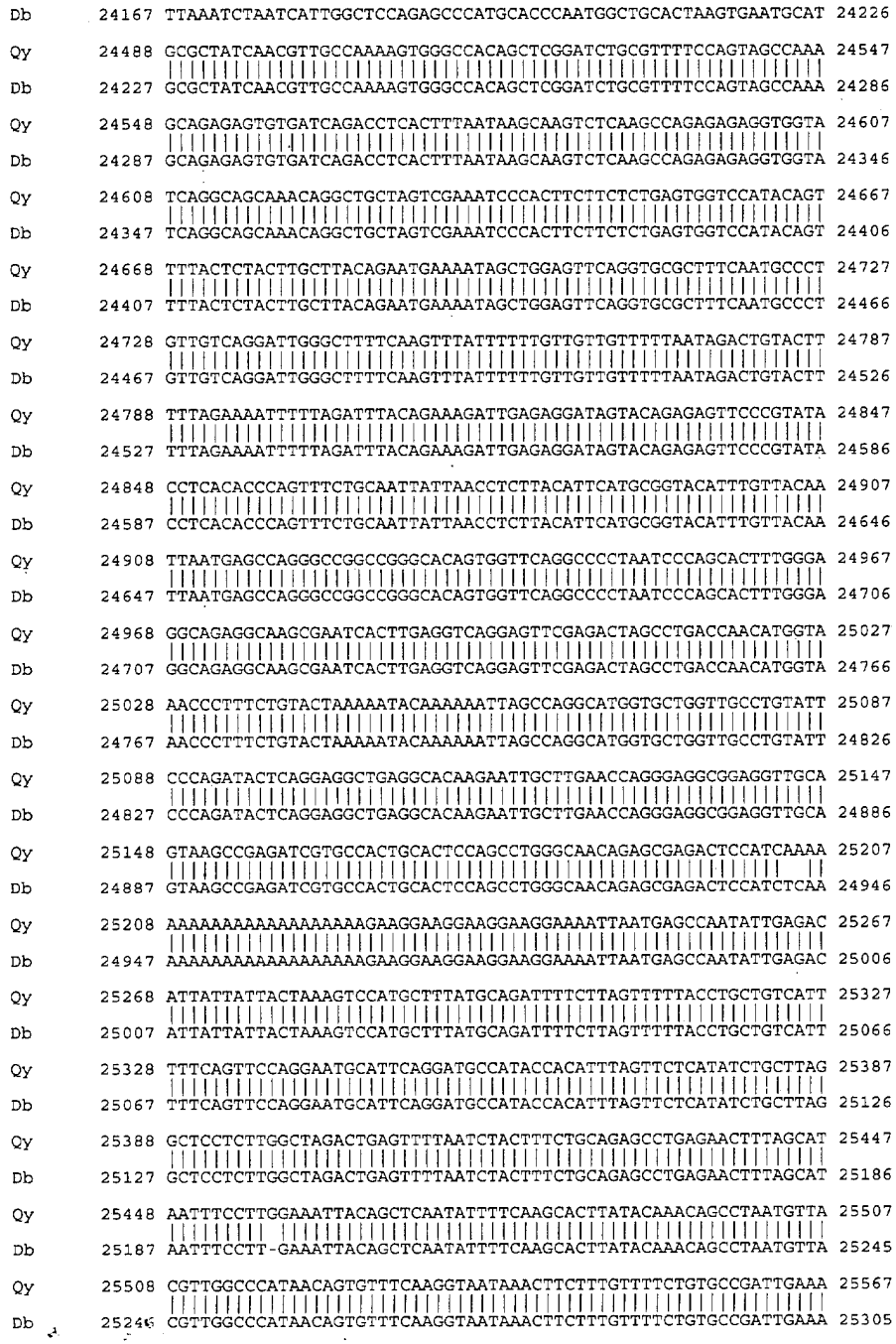
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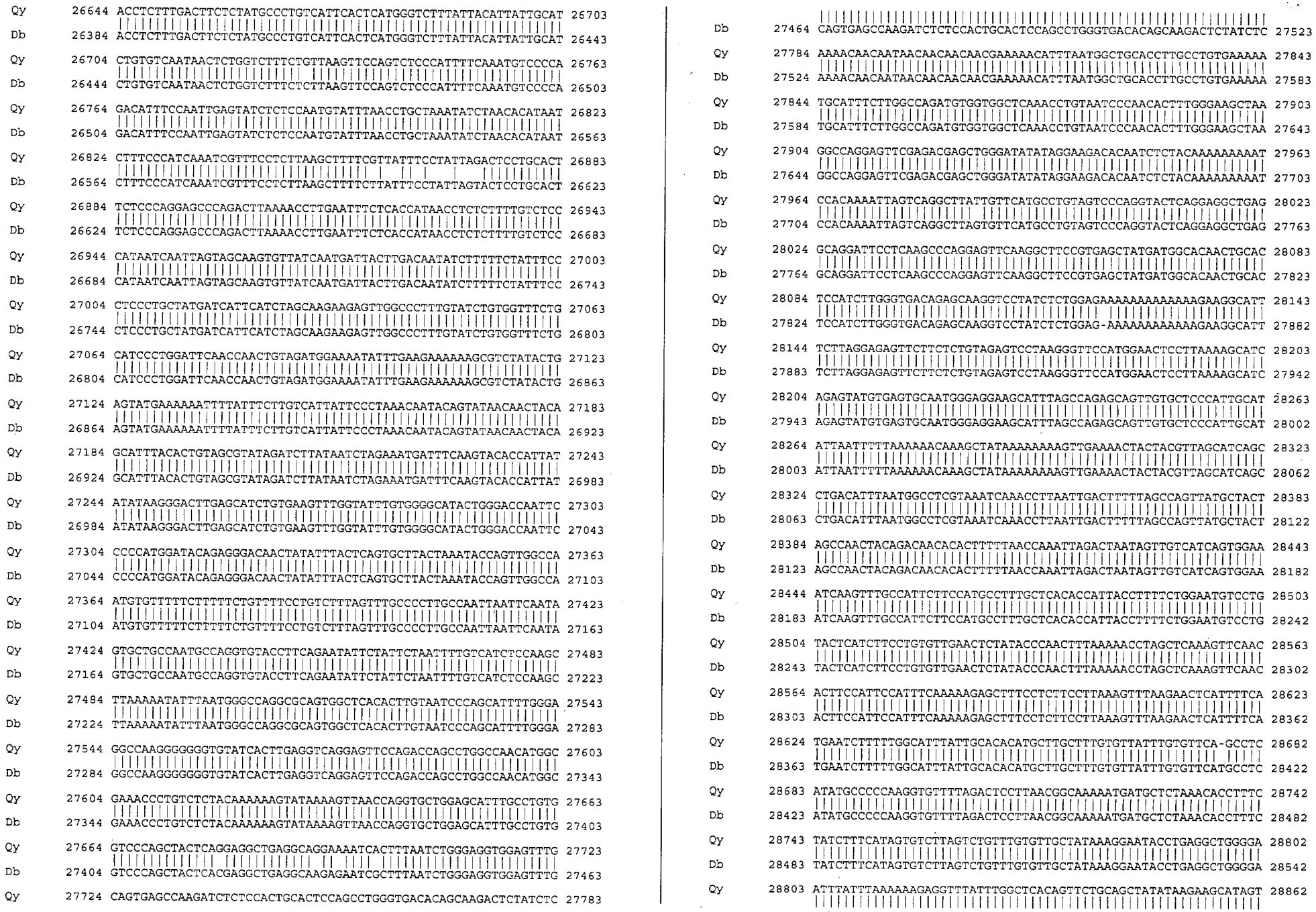
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Qy      32337 GTAGGGGTGGAGTTCCCTTCACTTCTAGAAGGCCCTGGATTAGTATCCCAGAGCTGTCAT 32396
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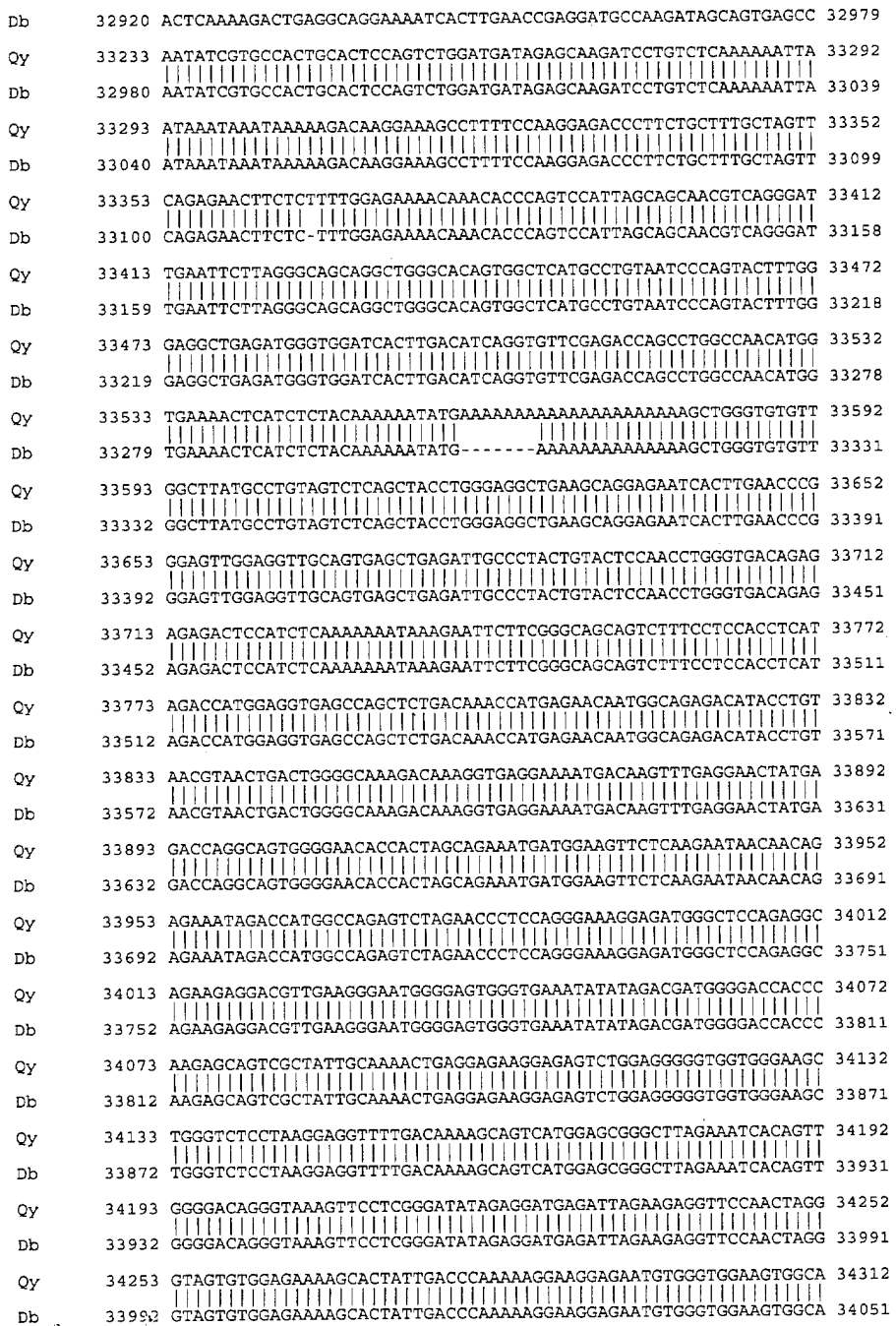
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Qy      32993 CAAGGAAAGGCCAAGTGCAGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAAATTGAGG 33052
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Qy      36592 TTTTCCCCAGTTGGTTGCACTCAAGCTGAGAGCAAAGCAATTGCACTTTAAATCCCCTTA 36651
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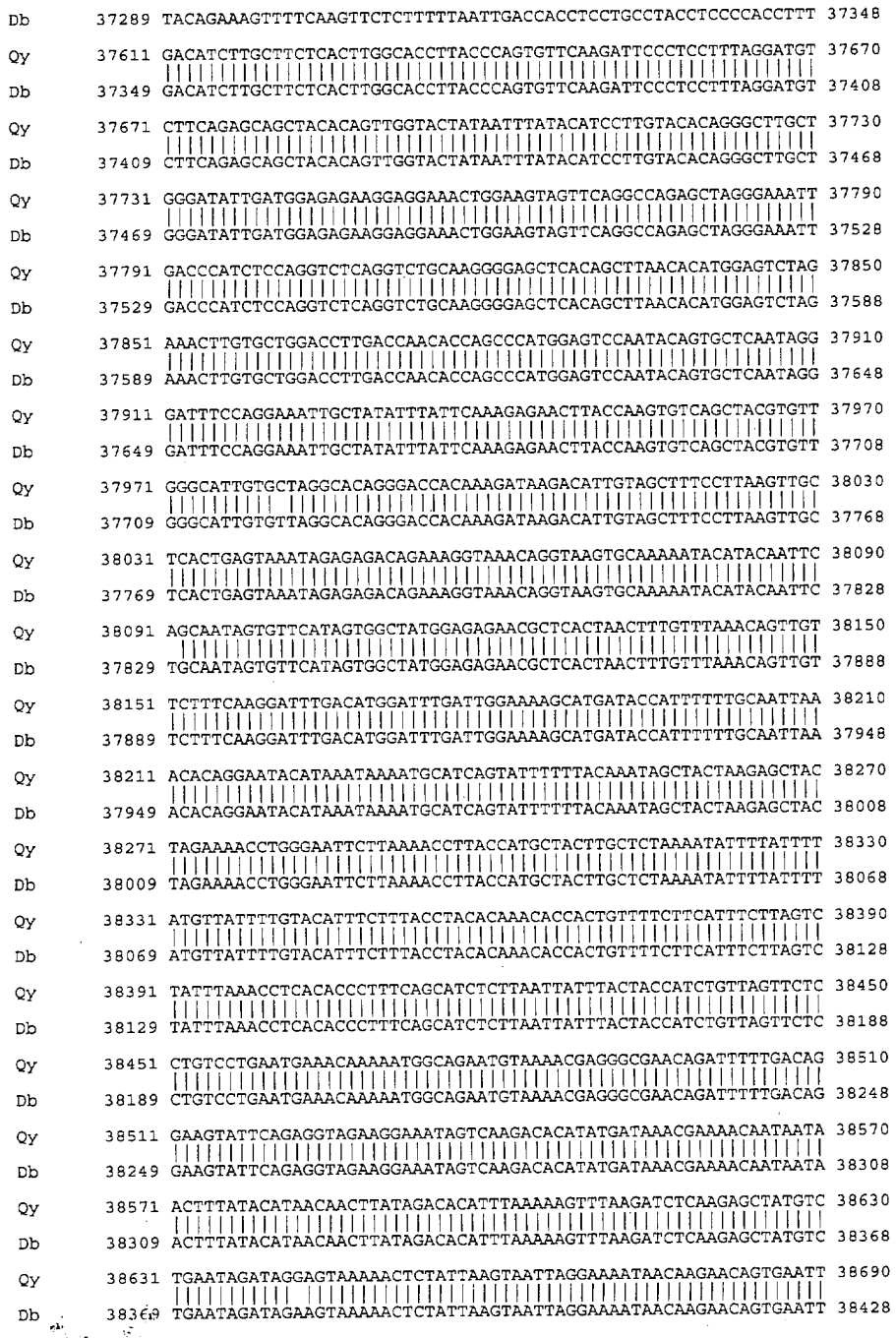
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RESULT 7
AF042484
LOCUS AF042484 80155 bp DNA linear PRI 22-JUN-2000
DEFINITION Homo sapiens sequence of the 80 kb core centromere protein binding region of the mar del(10) neocentromere corresponding to human chromosome 10q25.2, complete sequence.
ACCESSION AF042484
VERSION AF042484.1 GI:4205782
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 80155)
AUTHORS Barry,A.E., Howman,E.V., Cancilla,M.R., Saffery,R. and Choo,K.H.
TITLE Sequence analysis of an 80 kb human neocentromere
JOURNAL Hum. Mol. Genet. 8 (2), 217-227 (1999)
MEDLINE 99135901
PUBMED 9931329
REFERENCE 2 (bases 1 to 80155)
AUTHORS Barry,A.E., Howman,E.V., Cancilla,M.R., Saffery,R. and Choo,A.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-1998) Chromosome Research Unit, The Murdoch Institute, 10th Floor, Royal Childrens Hospital, Flemington Rd., Parkville, Melbourne, Victoria 3052, Australia
FEATURES Location/Qualifiers

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  Matches 39445;  Conservative    0;  Mismatches  139;  Indels   95;  Gaps   52;

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Qy        443 TAAGTTTTAGATGTTATGTTTCCTTATACTTAAAGTGGGTGTCTTATAGGCAGCATATAT 502
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        803 CAAATAGTATTTTACCAGCTCAAGTGTAATGTAGAAACCTTACAAGAGTATATTTTCATT 862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAAATAGTATTTTACCAGCTCAAGTGTAATGTAGAAACCTTACAAGAGTATATTTTCATT 480

Qy        863 TCTGTCTCCTAATTTTTATGCTA-TGTCTATAATACATTAGGTTTGTTGTTGTTTGTTTT 921
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
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Qy        922 TACCTTATTGCTGTTGGCTGGGGTCAGCAAACATTTTCTGTAAAGGGCTAGATAGTACAG 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TACCTTATTGCTGTTGGCTGGGGTCAGCAAACATTTTCTGTAAAGGGCTAGATAGTACAG 600

Qy        982 GCATACCTTGGAGATACTGTGGGTTTGGTTCCATACCACCACAATAATACAAATATGCAA 1041
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Db        601 GCATACCTTGGAGATACTGTGGGTTTGGTTCCATACCACCACAATAATACAAATATGCAA 660

Qy       1042 GAAGTGGATATCACAATAAAGTGAGTCACACAAGTCTTTTGGCTTCCCAGTGCATATAAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1102 AGTTTTGCTTATACTACACTGTAGTCTGTTAAGTGTGCAATAGTGTTATGTCTAAAAAAA 1161
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1162 CACATACCTTAATTTTAAAATGCTTTATTACTAAAAAATGCTAACAATCATTTGAGCATT 1221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACATACCTTAATTTTAAAATGCTTTATTACTAAAAAATGCTAACAATCATTTGAGCATT 840

Qy       1222 CAGTGAGTTGTAATCTTTTTGCTGGTGGAAGGTCTTTTCTTATTGATGACTGATCGGGGG 1281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGTGAGTTGTAATCTTTTTGCTGGTGGAAGGTCTTTTCTTATTGATGACTGATCGGGGG 900

Qy       1282 TCAGGTGCTGAAGCTTAGGGTGGCTGTGGCAGTTTCTTAAAACAACAGTGAAGATTGCAA 1341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCAGGTGCTGAAGCTTAGGGTGGCTGTGGCAGTTTCTTAAAACAACAGTGAAGATTGCAA 960

Qy       1342 TATCAGTTGACTCTTCCTTTCATGAAAGATTTCTCTCTAGTGTGTGATGCTTTTTGATAG 1401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TATCAGTTGACTCTTCCTTTCATGAAAGATTTCTCTCTAGTGTGTGATGCTTTTTGATAG 1020
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Qy    1402 CATTTTATGCACAGTAGAACTTCTTTGAAAATTGGA-TCAATCCTCTCAAACCCTGCTCT 1460
           ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
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Qy    1461 GCTTTAACAACCTAAGTTAATATAATATTCTGAATCCATTGTTGTCATTTCAACAATTTT 1520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GCTTTAACAACCTAAGTTAATATAATATTCTGAATCCATTGTTGTCATTTCAACAATTTT 1140

Qy    1521 CACAGTGTCTTCACCAGGAGTAGATTCCATCTCATTTCCTGAGATGGAATCTTTGCTCAT 1580
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Qy    1581 CCATAAGAAGAAATTCCTCATCTGTTCAAGTTTTATCATGAGATTGCAGCAATACAGTCA 1640
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Qy    1641 TGTCTTCAGGCCTCACTTCACTTTTAATTCCAGTTCTCTTGCTGTTTCTACCACATCTGT 1700
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Qy    1701 GGTTCCTTCCTCCATTGAAGTCTTGAACCTCTCCAAGTCATCCATGAGGGTTGGAATCGA 1760
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Qy    1761 CTTCTTCCAAATTCCTGTTAATATTTATATTTTGACCTCCCATGAATCATGAATGTTCTT 1820
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Db    1381 CTTCTTCCAAATTCCTGTTAATATTTATATTTTGACCTCCCATGAATCATGAATGTTCTT 1440

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Qy    1881 ATCCATCCAGAGGATCCACTTTCAATGCCAGTTATAGCCTTATGGAATGTATTTCTTCAA 1940
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Db    1501 ATCCATCCAGAGGATCCACTTTCAATGCCAGTTATAGCCTTATGGAATGTATTTCTTCAA 1560

Qy    1941 TAATAAGGCTTGAAAGTTGAAATTACTCCTTGATCCATTTTCTGCAAAATAGATGTTGTG 2000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TAATAAGGCTTGAAAGTTGAAATTACTCCTTGATCCATTTTCTGCAAAATAGATGTTGTG 1620

Qy    2001 TTAGCAGGCATGAAAGCAACATTAATCTTTTTGTACATGTCCATCAGAGCTCTTGGGTGA 2060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TTAGCAGGCATGAAAGCAACATTAATCTTTTTGTACATGTCCATCAGAGCTCTTGGGTGA 1680

Qy    2061 CCAGGTATATTGCCAGTGAGCAGTAATACTTTGAAAGGAATTATTTTTCTTAGCAGTAGG 2120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CCAGGTATATTGCCAGTGAGCAGTAATACTTTGAAAGGAATTATTTTTCTTAGCAGTAGG 1740

Qy    2121 TCTCAACAATGGGCTTAAAATATTTGGTCCACCATTCTGTAAACTGATGTGCTGTCATCT 2180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 TCTCAACAATGGGCTTAAAATATTTGGTCCACCATTCTGTAAACTGATGTGCTGTCATCT 1800

Qy    2181 AAACTTTGTAGTTTCATTTATAGAGCACAGGCAGAGTAGATGTAGCATAATTCTTAAGGG 2240
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Db    1801 AAACTTTGTAGTTTCATTTATAGAGCACAGGCAGAGTAGATGTAGCATAATTCTTAAGGG 1860

Qy    2241 ACTTAGGATTTTCAGAATGGTAAATGAACATTGGCATCAATTTAAATCACTAGCTGTATT 2300
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Db    1861 ACTTAGGATTTTCAGAATGGTAAATGAACATTGGCATCAATTTAAATCACTAGCTGTATT 1920

Qy    2301 AGCCCCCAACAAGAGAGTCAGCCTATTTTTTGAAGCTTTGAAGCCAAGCGTCGACTTCTC 2360
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Db    1921 AGCCCCCAACAAGAGAGTCAGCCTATTTTTTGAAGCTTTGAAGCCAAGCGTCGACTTCTC 1980

Qy    2361 CTCCCTGGTTACAAAAGTCCTAAATGGCATCTTCTTCCAATATAAGGCTGTTTTATCTAC 2420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CTCCCTGGTTACAAAAGTCCTAAATGGCATCTTCTTCCAATATAAGGCTGTTTTATCTAC 2040

Qy    2421 ATTGAAAATCTGTTGTTTAGTGTAGCCACCTTCATCAATGATACTATCTAGATCTCTTGG 2480
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    2041 ATTGAAAATCTGTTGTTTAGTGTAGCCACCTTCATCAATGATACTATCTAAATCTCTTGG 2100

Qy    2481 ATAACTTGTGCAGCTTCTACATCAGCATTTGCTACTTCACCTTGTACTCTTATGTAATGG 2540
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Db    2101 ATAACTTGTGCAGCTTCTACATCAGCATTTGCTACTTCACCTTGTACTCTTATGTAATGG 2160

Qy    2541 AGTGGCATCTTTCCTCGTACCTCATGAACCAACCTCTGCTAGCTTCCAACTTTTCTTCTG 2600
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Db    2161 AGTGGCATCTTTCCTCGTACCTCATGAACCAACCTCTGCTAGCTTCCAACTTTTCTTCTG 2220

Qy    2601 TAGTTTCCTCGCCTCTCTCAGCCTTCATAGACTTGAGGATAGTTAGAGACTTGCTTTGGA 2660
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Qy    2661 TTAGATTTTGGCTTCAGGAAATGTTGTGGCTGGTTTGATCTTCTATCCAGACCACTAAAA 2720
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Db    2281 TTAGATTTTGGCTTCAGGAAATGTTGTGGCTGGTTTGATCTTCTATCCAGACCACTAAAA 2340

Qy    2721 CTTTATCCATATCAGCAATAAGGCTGTTTTGCTTTCTTATTATTTGTGTGTTCACTGGAG 2780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 CTTTATCCATATCAGCAATAAGGCTGTTTTGCTTTCTTATTATTTGTGTGTTCACTGGAG 2400

Qy    2781 TAGCACTTTTAATTTGCTTCAAGATATATTTCTTTGCATTCACAACTTGGCTGACTGGTG 2840
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Db    2401 TAGCACTTTTAATTTGCTTCAAGATATATTTCTTTGCATTCACAACTTGGCTGACTGGTG 2460

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Db    2581 GCATATGCCTGTAATTCCAACACATTAAGAGGCCAAGGTGGGAGGATTGCTTGAACCCAG 2640

Qy    3021 GAGGTGGAGGTTGTAGAGATCACACCACTGCATTCCGTCCTGGATGACAGAGCAAGA-CC 3079
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    2641 GAGGTGGAGGTTGTAGAGATCACACCACTGCATTCCGTCCTGGATGACAGAGCAAGACCC 2700

Qy    3080 TTTCTCAAAATAAAATGAGAGGTGTGCTTCTTCTTTTTGTTTGAGCCCATAGAAGCCATA 3139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    3140 GTATGATTTTTAATTGGCCTAATTTCAATACTGTTGTGTCTCAGAGAATAGGGAGGTCTG 3199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    3200 AAGAGAGGGAGAGAGGTGGGGGAATGGCTGGTCAGTGGAGCAGTCAGAACACACATAACA 3259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 AAGAGAGGGAGAGAGGTGGGGGAATGGCTGGTCAGTGGAGCAGTCAGAACACACATAACA 2880

Qy    3260 CTAATAAATTGTTTGCTGTCTTATATGGATGTGGTTTGTGATGCCCCCAAACAATTACAA 3319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 CTAATAAATTGTTTGCTGTCTTATATGGATGTGGTTTGTGATGCCCCCAAACAATTACAA 2940

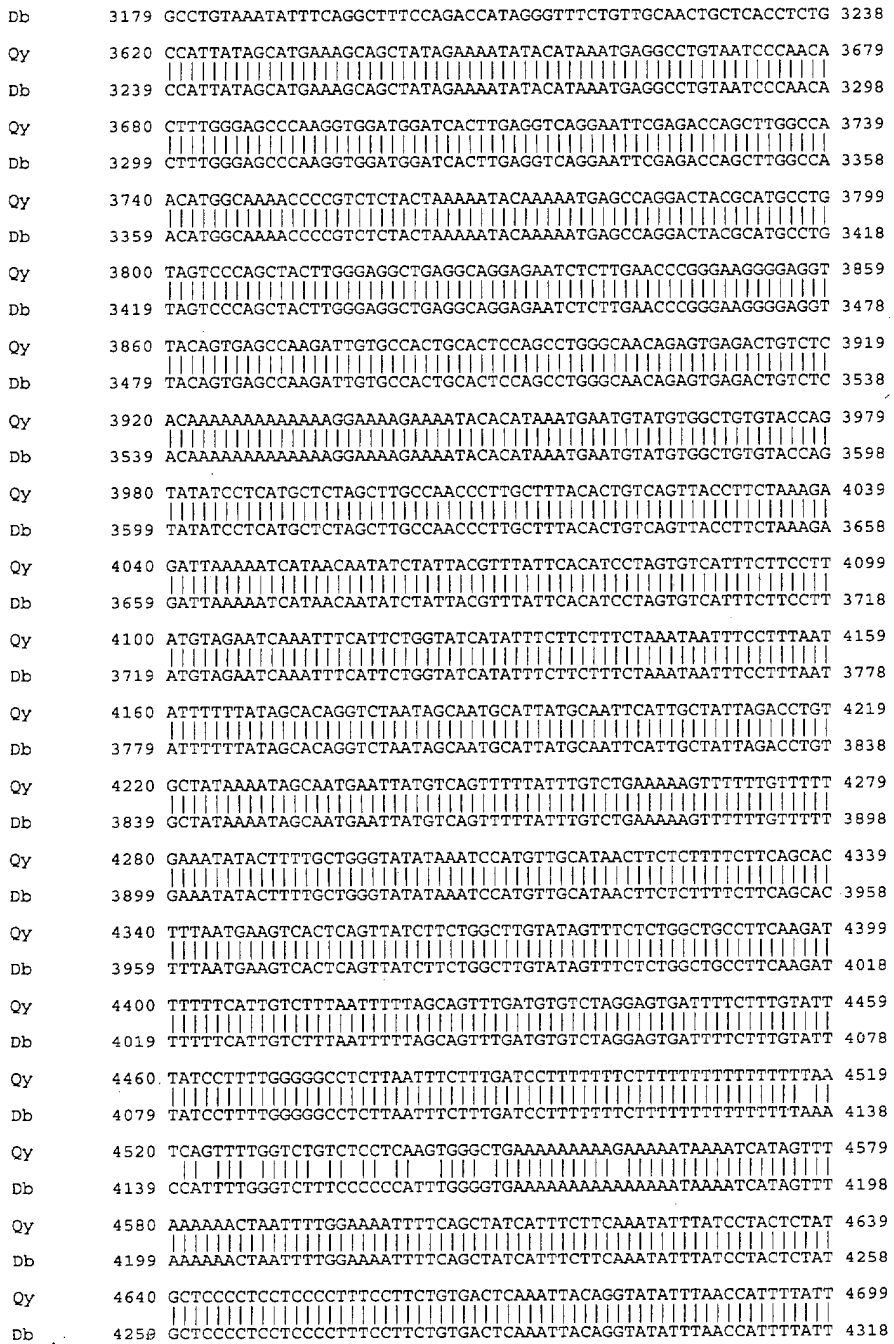
Qy    3320 TAGTTACAGCAAATATCACTGATCACAGATCACCATAACAGATATAAGAATCATGGCAAA 3379
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    2941 TAGTTACAGCAAATATCACTGATCACAGATCACCATAACAGATATAAGAATCATGGAAAA 3000

Qy    3380 GTTTGAAATATTCTTGAGAATTAGCAAAGTGTGACACAGAGAAACAAAGTGAGCACATGC 3439
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 GTTTGAAATATT-TTGAGAATTAGCAAAGTGTGACACAGAGAAACAAAGTGAGCACATGC 3059

Qy    3440 CGTTGGAAAAAAATTGGTGTTGATAGACTTGCTCCATCGCAAGTTTGCCATACGCCTTCAA 3499
           |||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db    3060 TGTTGGAAAAAAATTGGTGTTGATAGACTTGCTCCAT-GTAAGTTTGCCATACGCCTTCAA 3118

Qy    3500 TTTATAAAAAACACAATATCTAGGAAGTTCAATAAAGTGAAGTGCAATAAGATGAAGTAT 3559
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Db    3119 TTTATAAAAAACACAATATCTAGGAAGTTCAATAAAGTGAAGTGCAATAAGATGAAGTAT 3178

Qy    3560 GCCTGTAAATATTTCAGGCTTTCCAGACCATAGGGTTTCTGTTGCAACTGCTCACCTCTG 3619
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Db 3179 GCCTGTAAATATTTCAGGCTTTCCAGACCATAGGGTTTCTGTTGCAACTGCTCACCTCTG 3238
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Db 3239 CCATTATAGCATGAAAGCAGCTATAGAAAATATACATAAATGAGGCCTGTAATCCCAACA 3298
Qy 3680 CTTTGGGAGCCCAAGGTGGATGGATCACTTGAGGTCAGGAATTCGAGACCAGCTTGGCCA 3739
Db 3299 CTTTGGGAGCCCAAGGTGGATGGATCACTTGAGGTCAGGAATTCGAGACCAGCTTGGCCA 3358
Qy 3740 ACATGGCAAAACCCCGTCTCTACTAAAAATACAAAAATGAGCCAGGACTACGCATGCCTG 3799
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Qy 4400 TTTTTCATTGTCTTTAATTTTTAGCAGTTTGATGTGTCTAGGAGTGATTTTCTTTGTATT 4459
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Qy 4460 TATCCTTTTGGGGGCCTCTTAATTTCTTTGATCCTTTTTTTCTTTTTTTTTTTTTTTTAA 4519
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Qy      5767 CATGGAGTAAGAGGGTGTTTTTTTTAGTTTTCATCCTCCAGCCTTGGTCTTGGGCCCTGAG 5826
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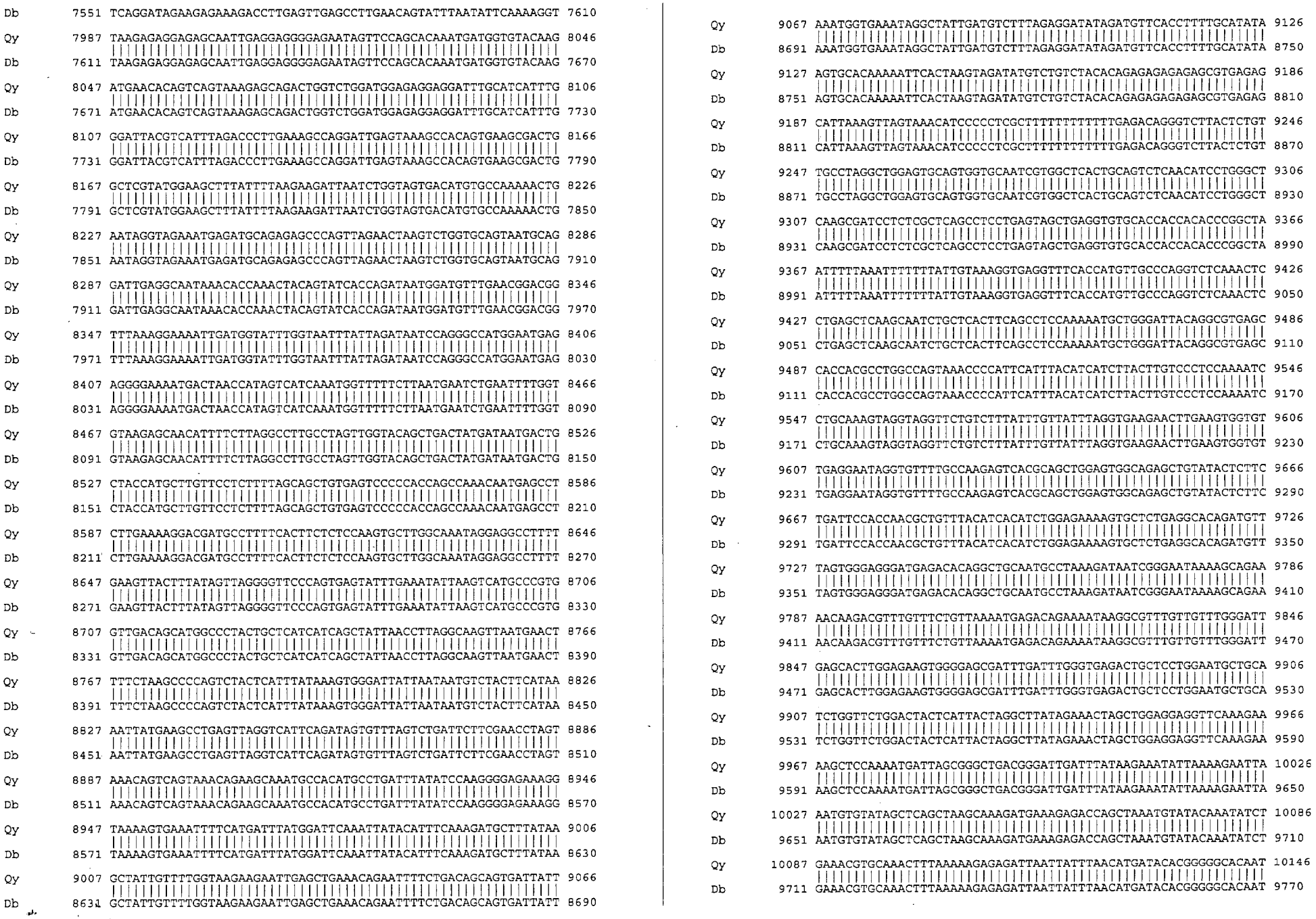
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Qy      7747 TAATGGGAACTCAAGAAGTGTACATATAAGGAGGGAAGTAGCAGTATGGTACAAGATAAT 7806
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Db      7431 ACATACATATCAGTGAATGATATTGCCAAAAAGTGCTATTGATAGAGCAATAATTCATTT 7490

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Db      7491 CTGCAAACAGCTGCTGATCTCCTACTGAAAACAGAGGAGGGAGAACAGGACGCCTCGTGG 7550

Qy      7927 TCAGGATAGAAGAGAAAGACCTTGAGTTGAGCCTTGAACAGTATTTAATATTCAAAAGGT 7986
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Db 7611 TAAGAGAGGAGAGCAATTGAGGAGGGGAGAATAGTTCCAGCACAAATGATGGTGTACAAG 7670
Qy 8047 ATGAACACAGTCAGTAAAGAGCAGACTGGTCTGGATGGAGAGGAGGATTTGCATCATTTG 8106
Db 7671 ATGAACACAGTCAGTAAAGAGCAGACTGGTCTGGATGGAGAGGAGGATTTGCATCATTTG 7730
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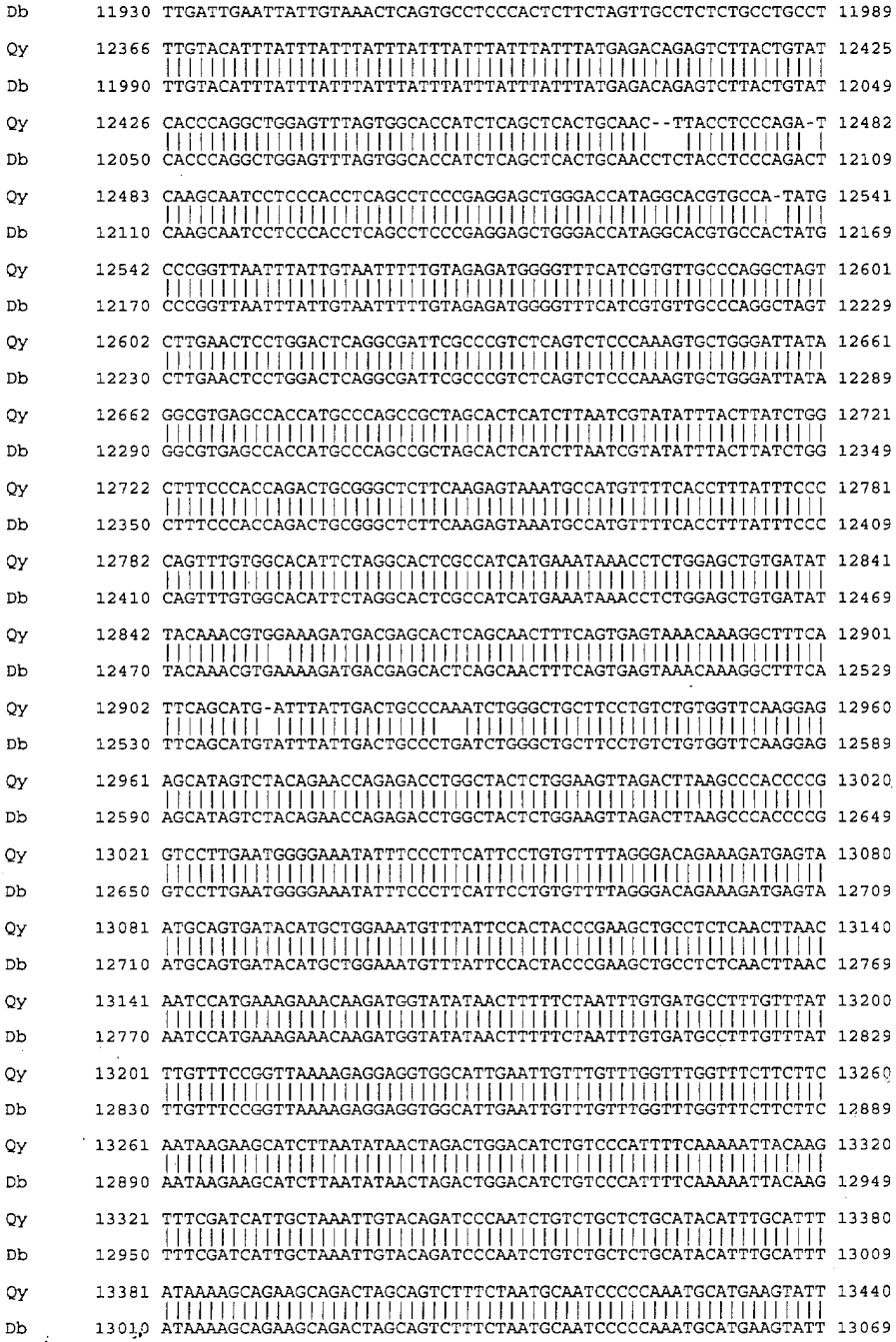
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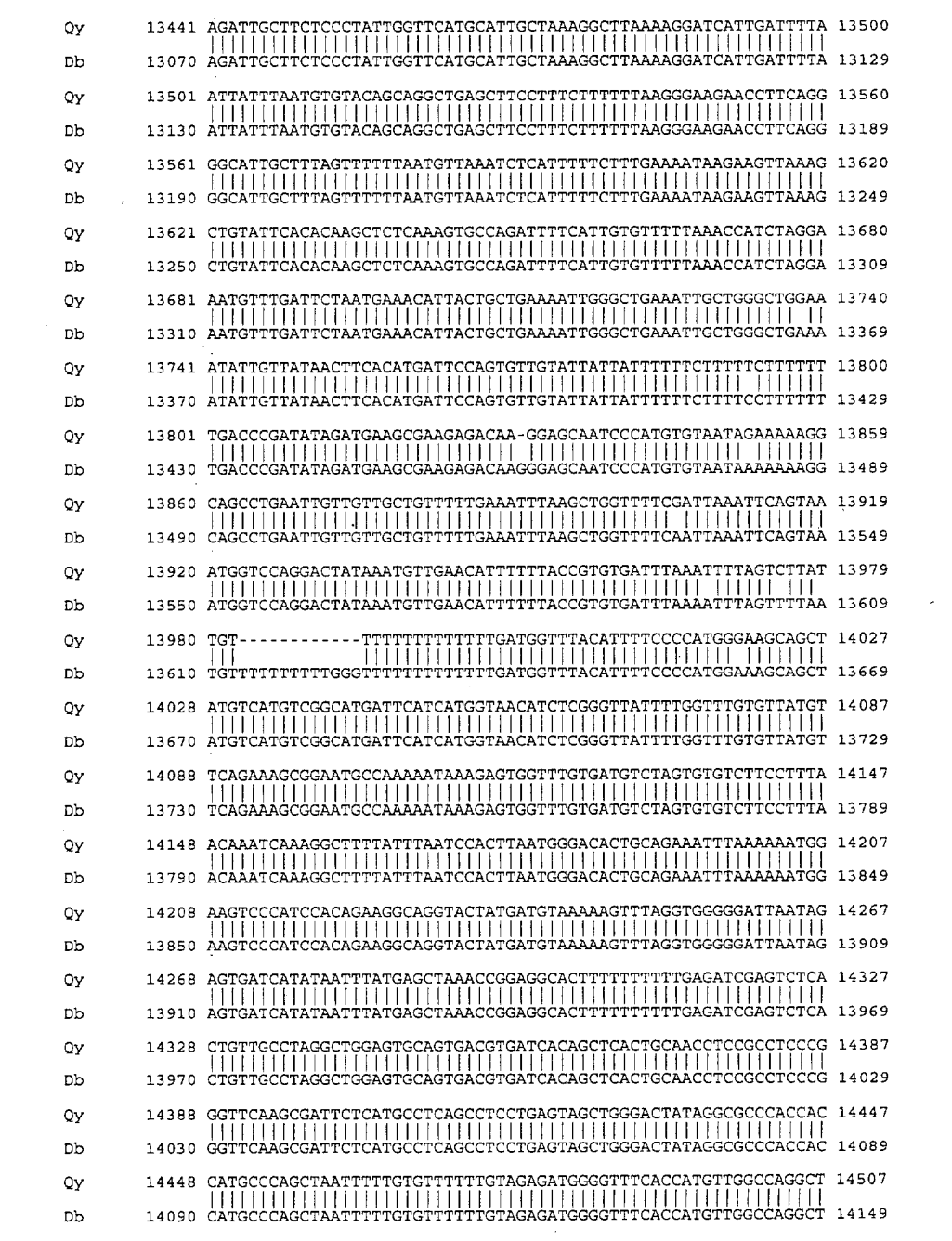
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Qy      12246 TACAGGGACTCCATCCCTTGTGCCCCACATACCTCACACGTAGACATTCCTAATGAAGAT 12305
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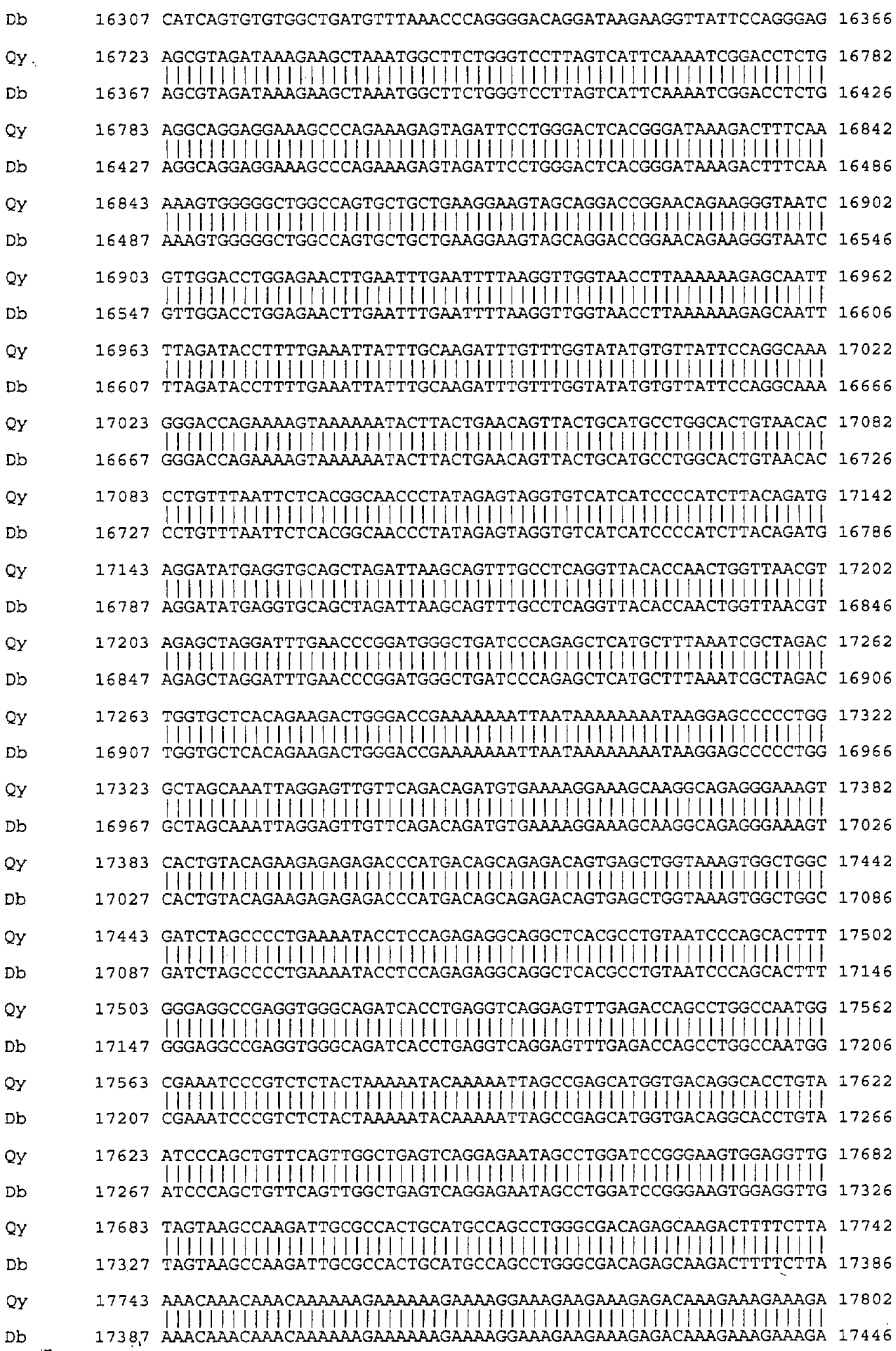
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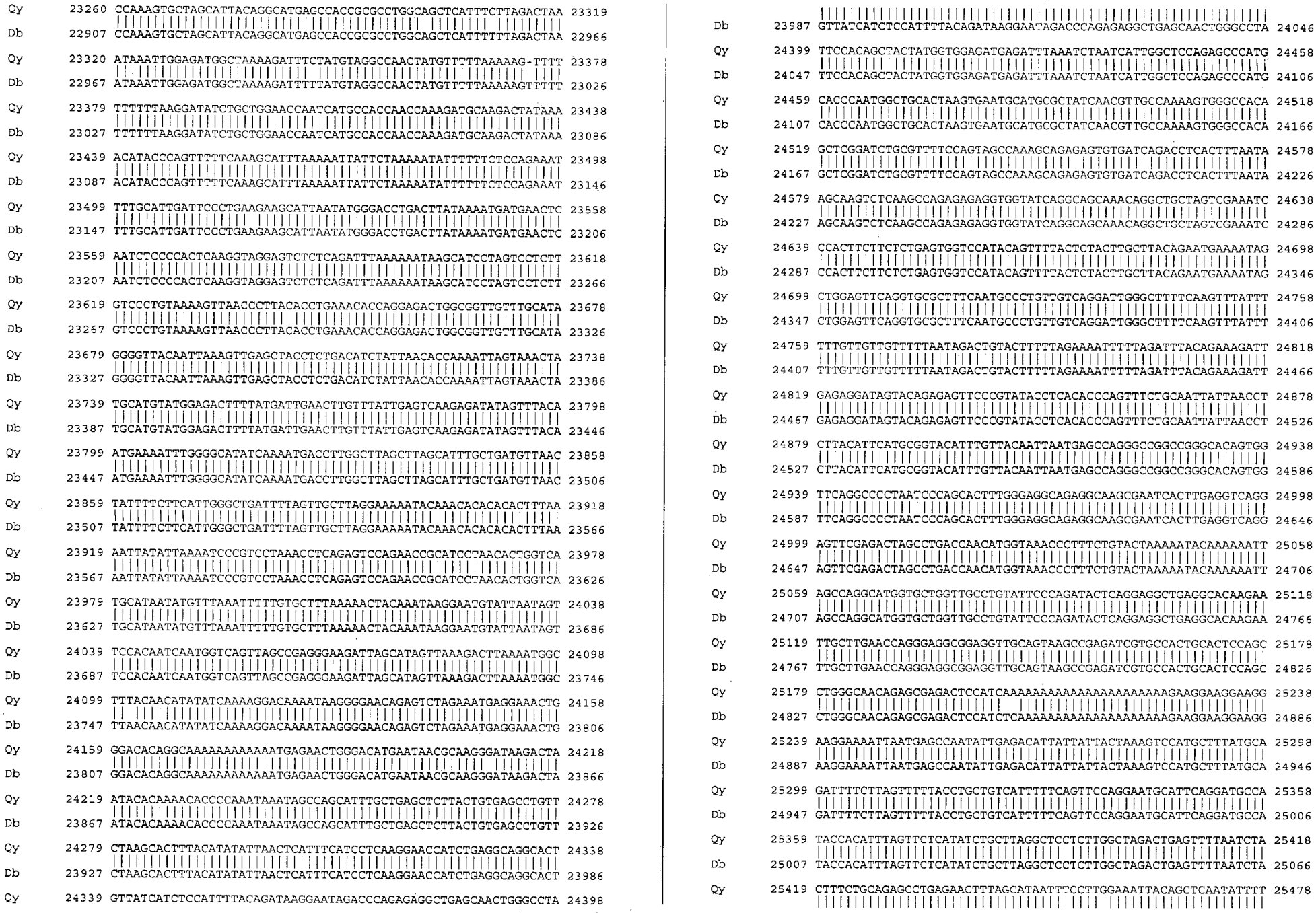
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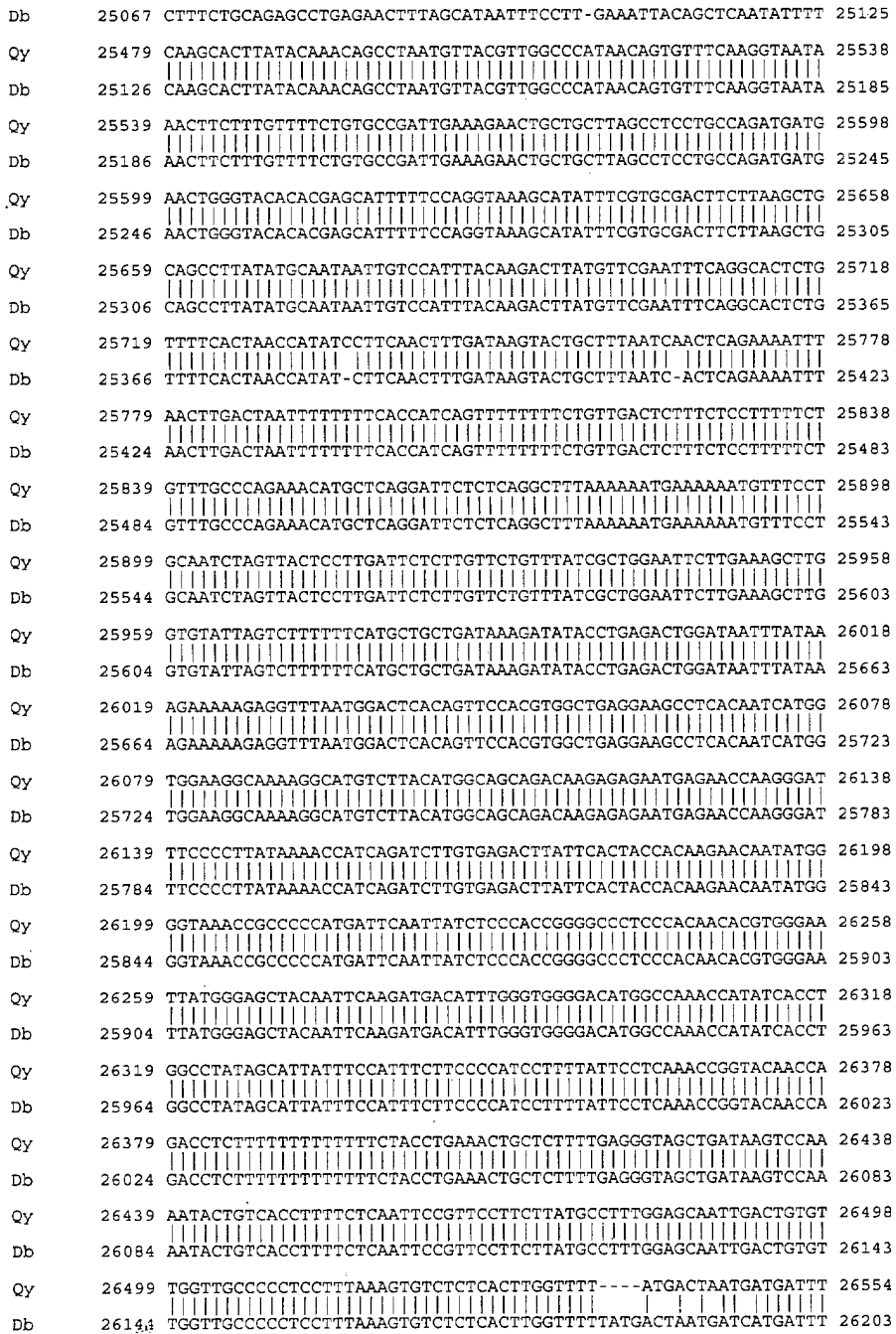
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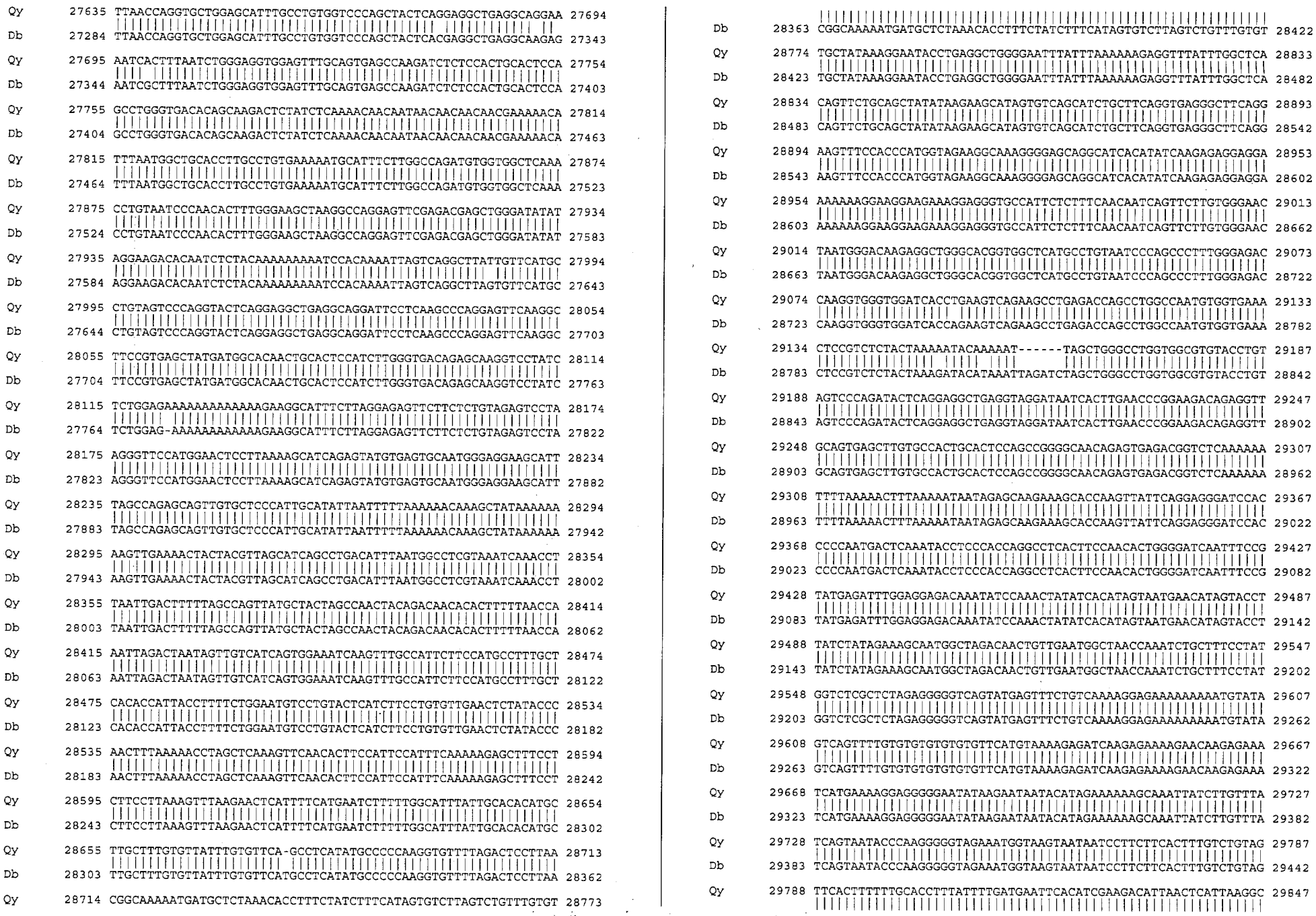
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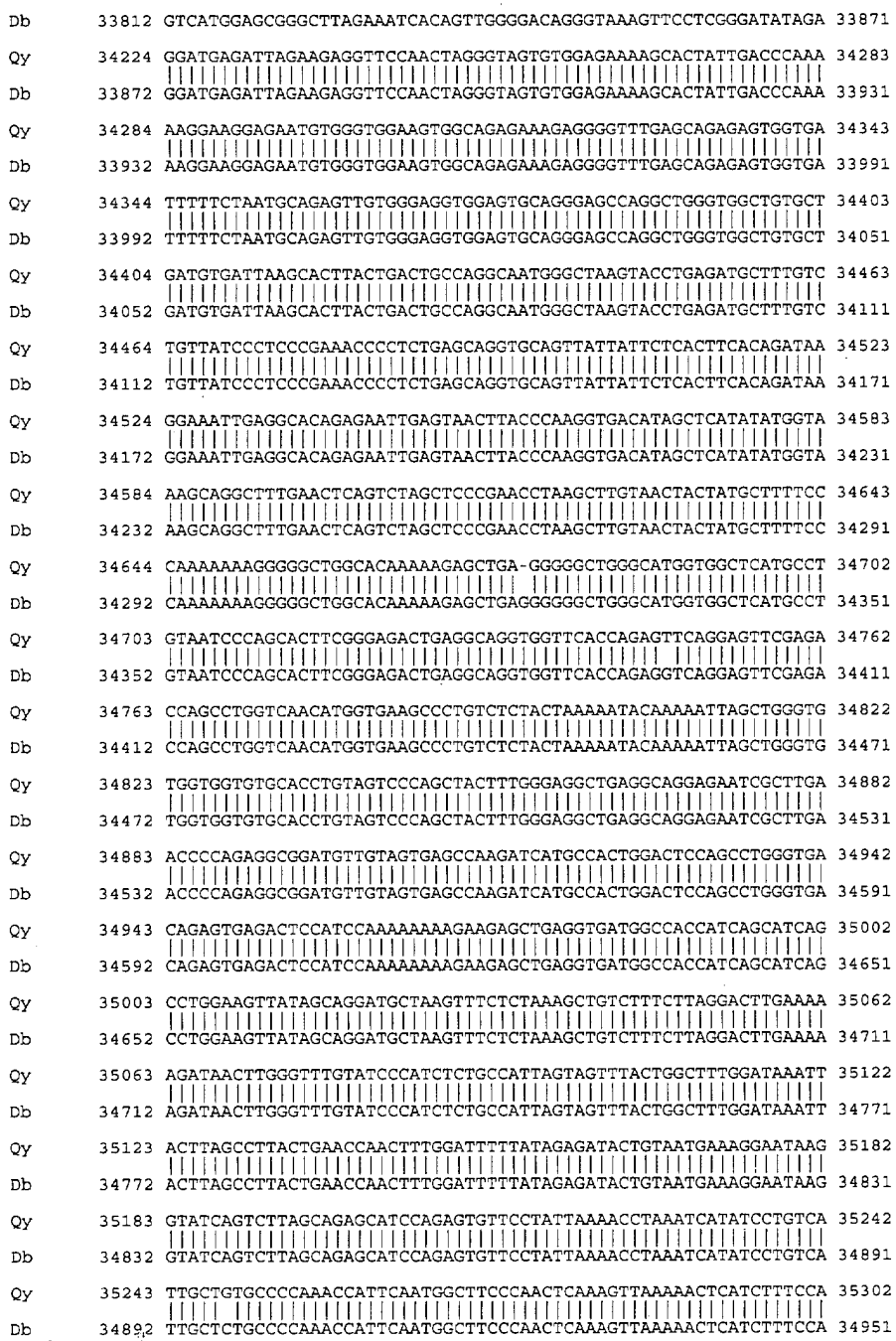
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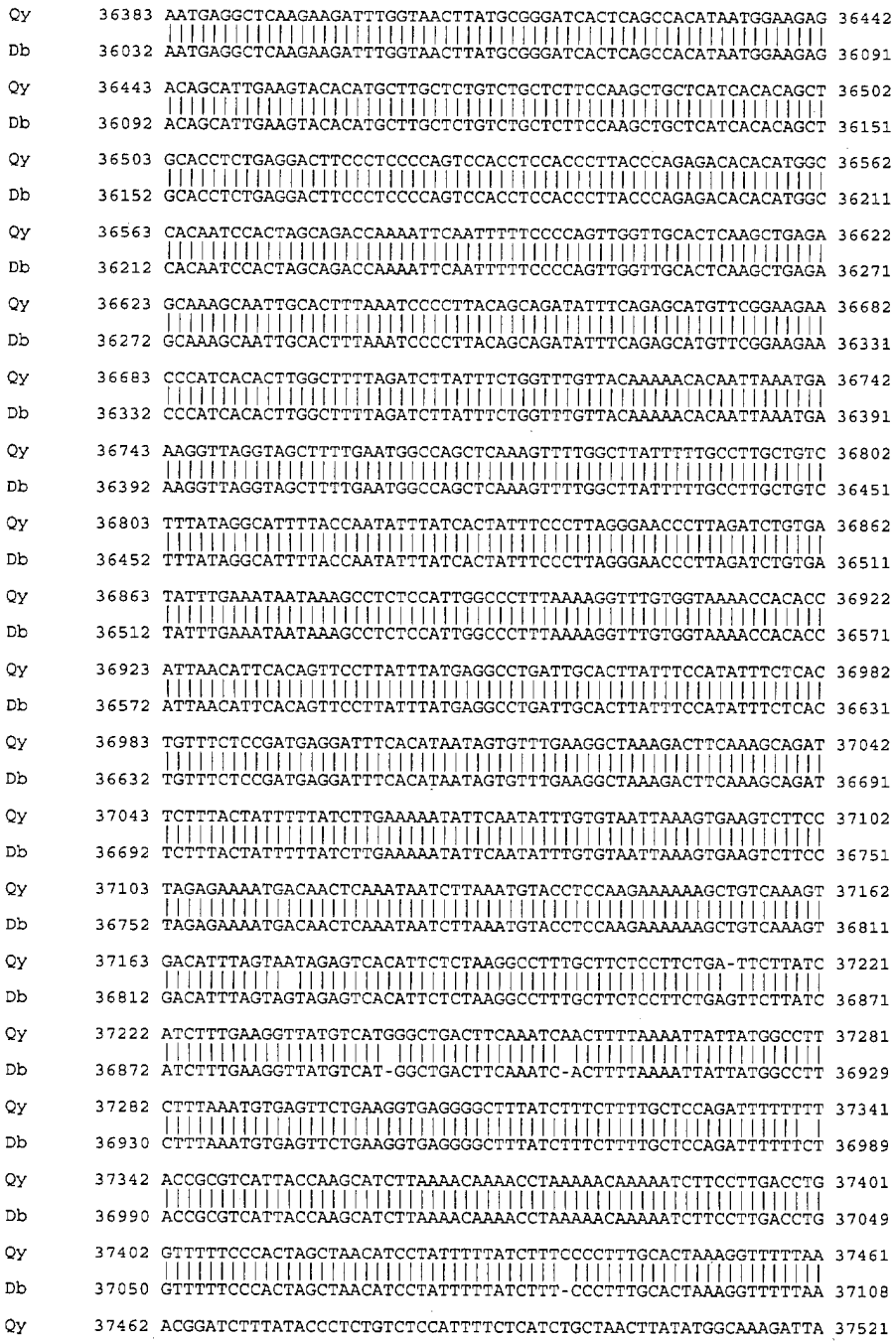
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Qy      38662 AATTAGGAAAATAACAAGAACAGTGAATTTCTTAATGAATGGCATGTAATCAAAACTGTA 38721
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RESULT 8
AL391648/c

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DEFINITION  Homo sapiens chromosome 10 clone RP11-203A7, 9 unordered pieces.
ACCESSION   AL391648
VERSION     AL391648.12  GI:14669309
KEYWORDS    HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Chapman,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Jul 10, 2001 this sequence version replaced gi:14596357.
            -------------- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            -------------- Project Information
            Center project name: bA203A7
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 174005 bases at least Q40
            Consensus quality: 174806 bases at least Q30
            Consensus quality: 175273 bases at least Q20
            Insert size: 175632; sum-of-contigs
            Insert size: 155595; 14.1% error; agarose-fp
            Quality coverage: 6.85x in Q20 bases; sum-of-contigs Quality
            coverage: 8.13x in Q20 bases; agarose-fp
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 9 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    23099: contig of 23099 bp in length
            *    23100    23199: gap of 100 bp
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            *    65531   100606: contig of 35076 bp in length
            *   100607   100706: gap of 100 bp
            *   100707   156710: contig of 56004 bp in length
            *   156711   156810: gap of 100 bp
            *   156811   159233: contig of 2423 bp in length
            *   159234   159333: gap of 100 bp
            *   159334   171732: contig of 12399 bp in length
            *   171733   171832: gap of 100 bp
            *   171833   174095: contig of 2263 bp in length
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ORIGIN

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  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches 39710;  Conservative    0;  Mismatches  177;  Indels  319;  Gaps   52;

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Qy         61 GCTAATTTTTGTATTTTAGTAGAGACGGGGTTTCACCGTGTTTGCCAGGCTGGTATCAAA 120
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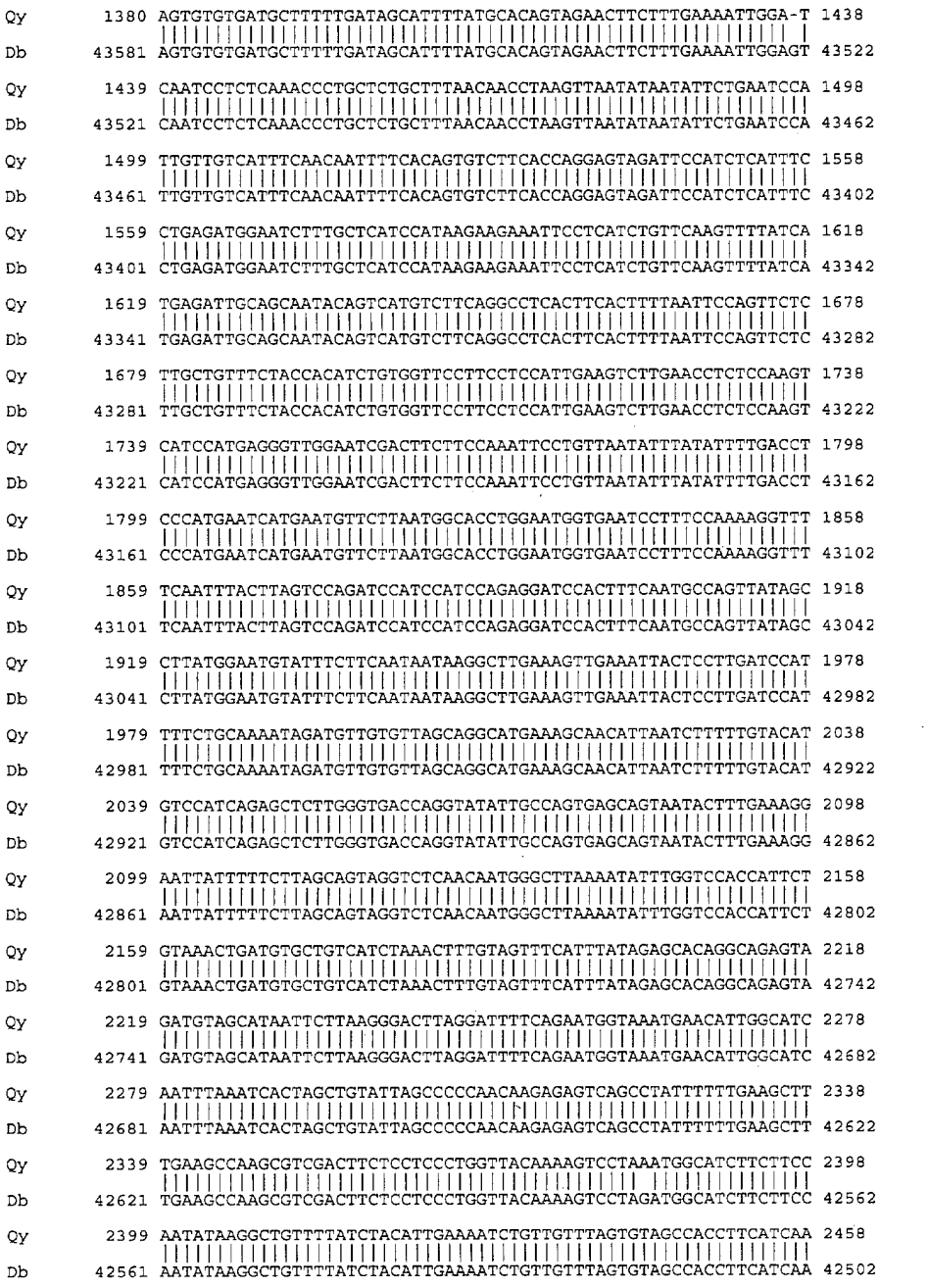
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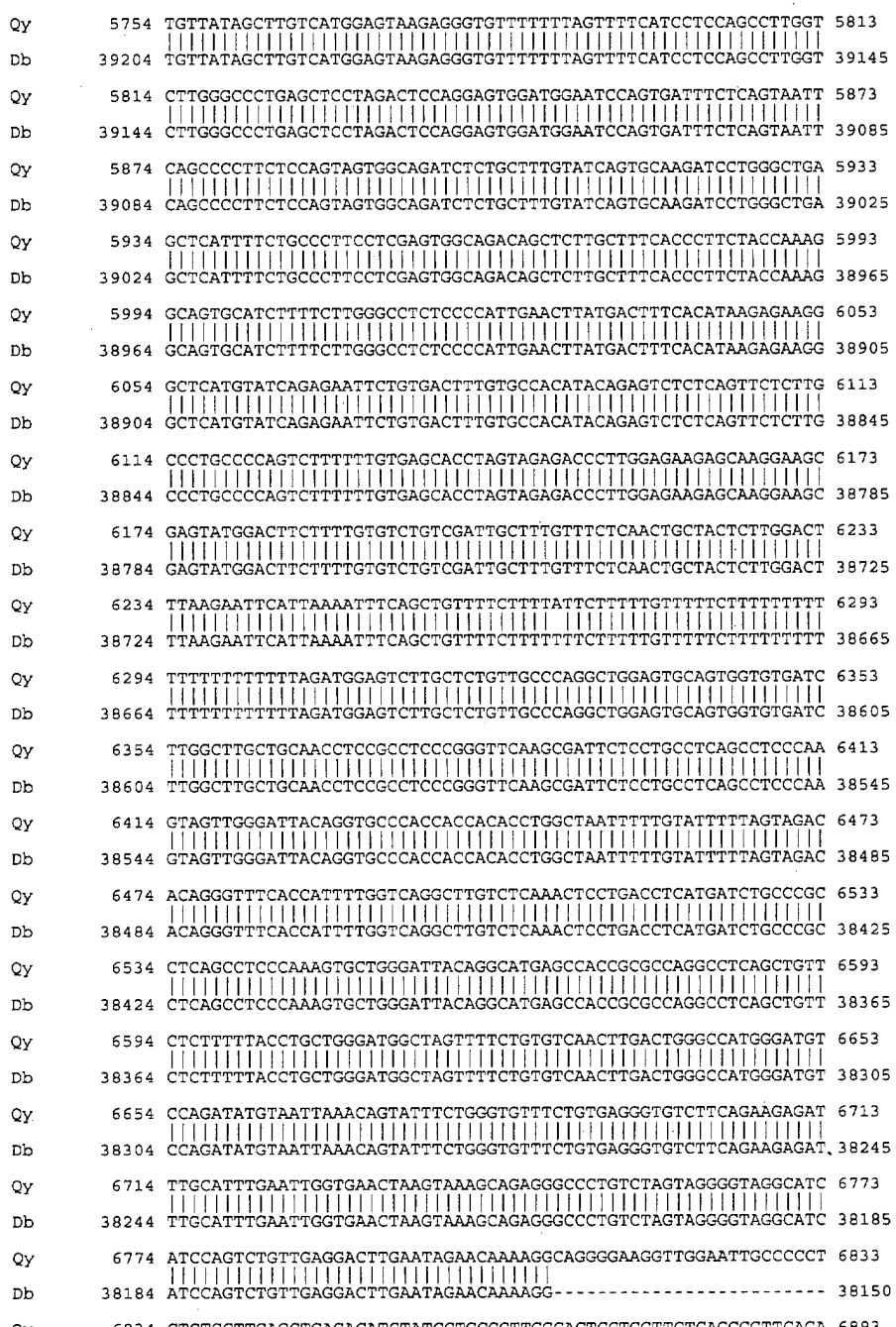
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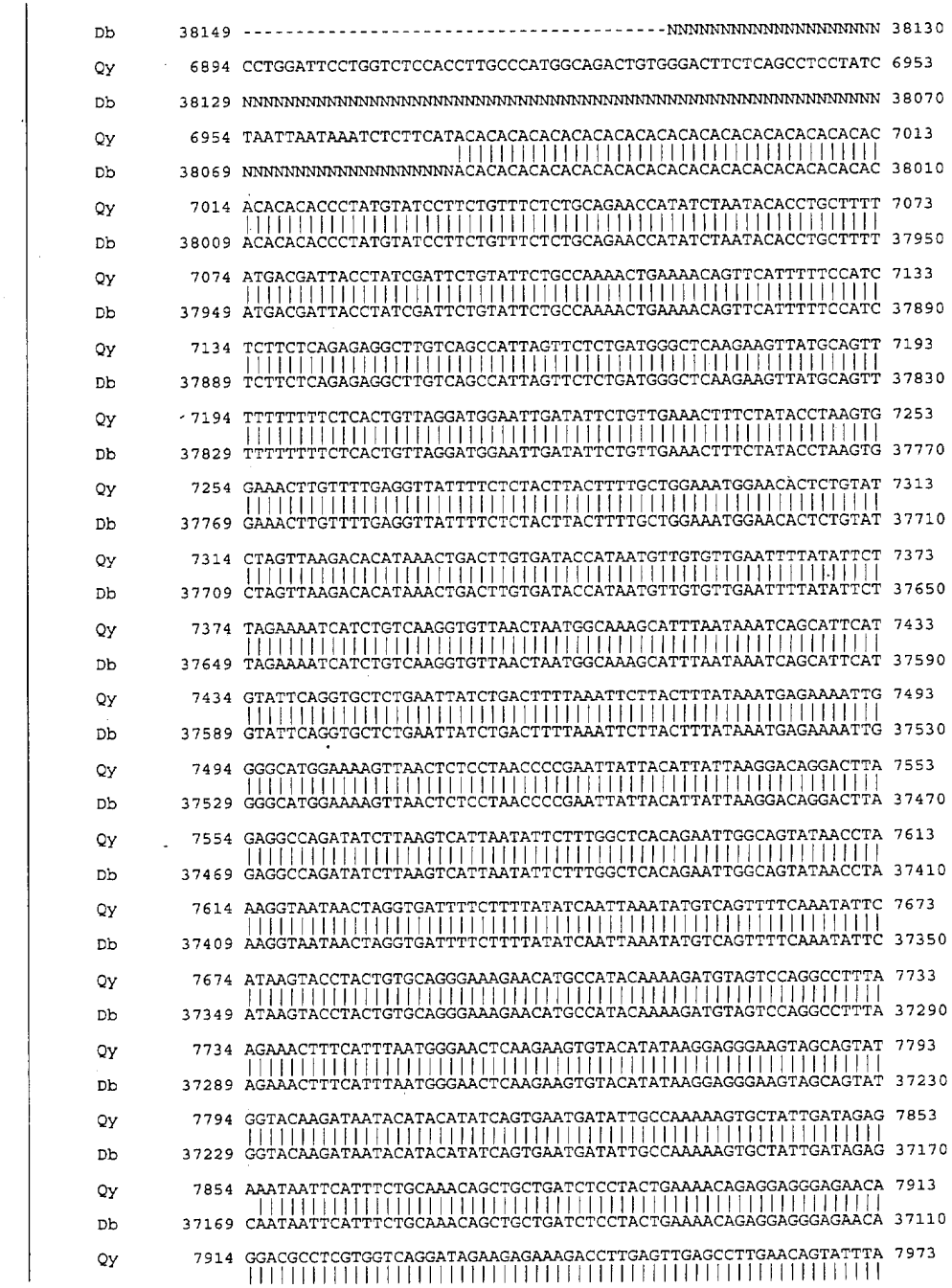
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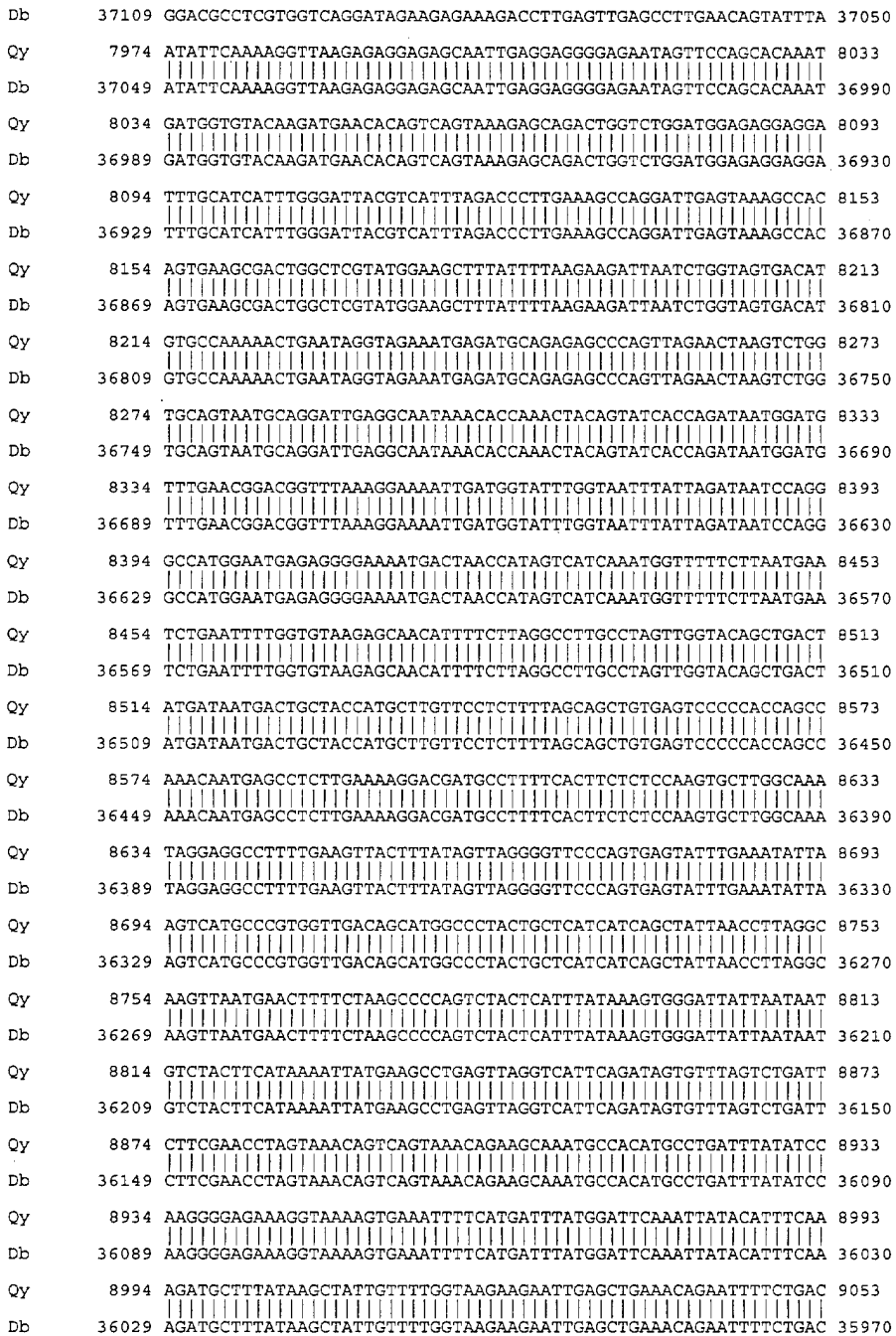

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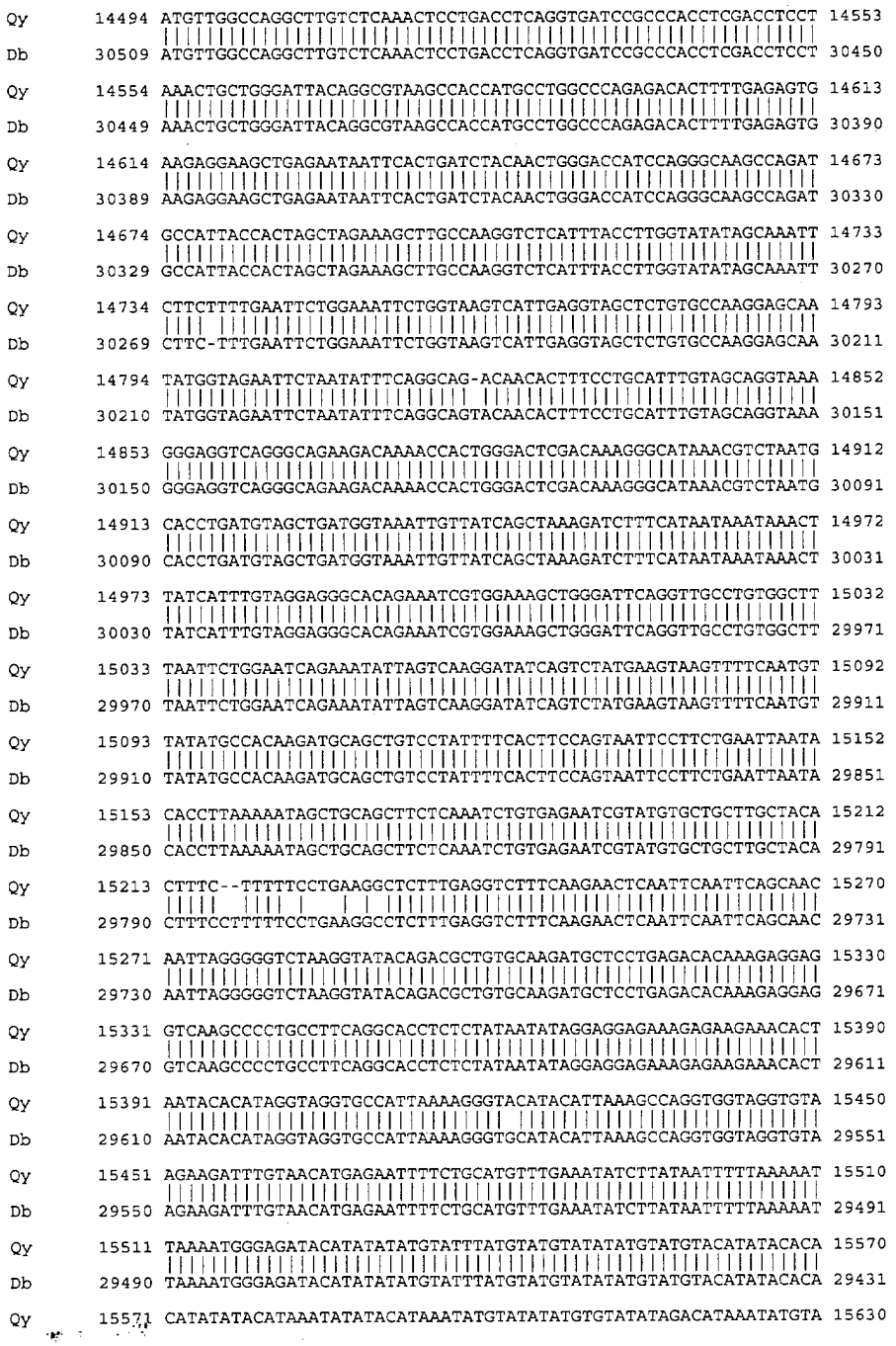

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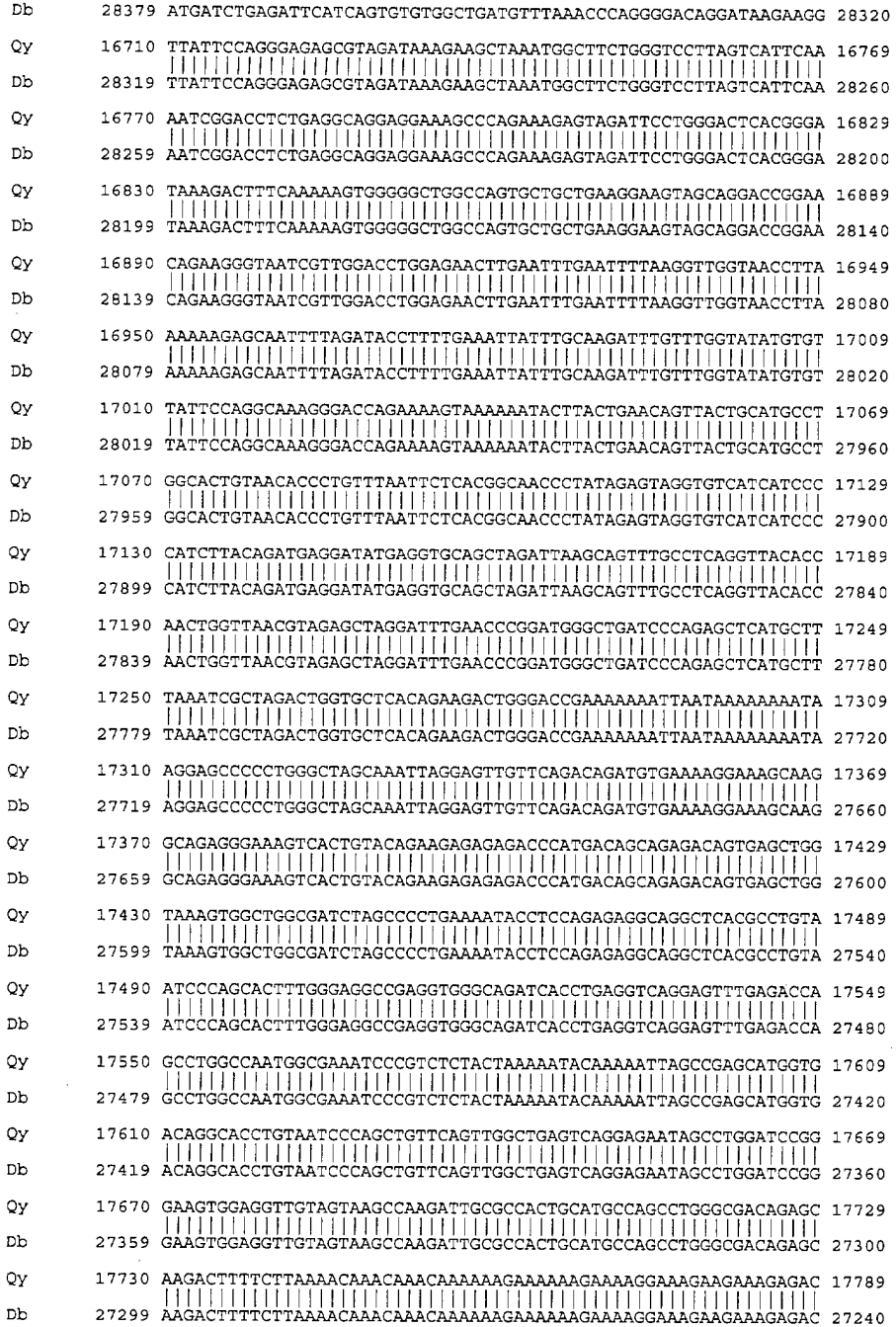

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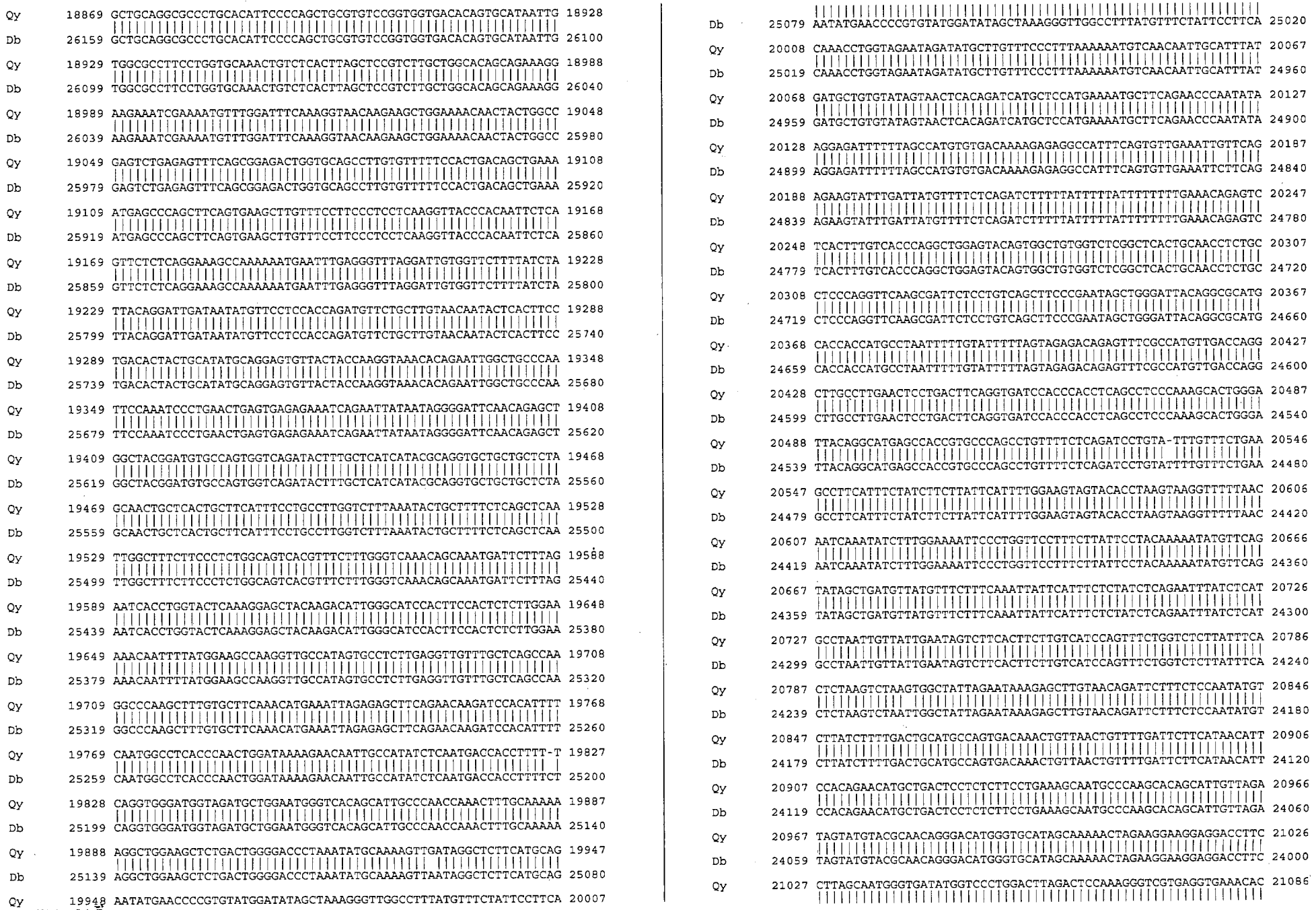


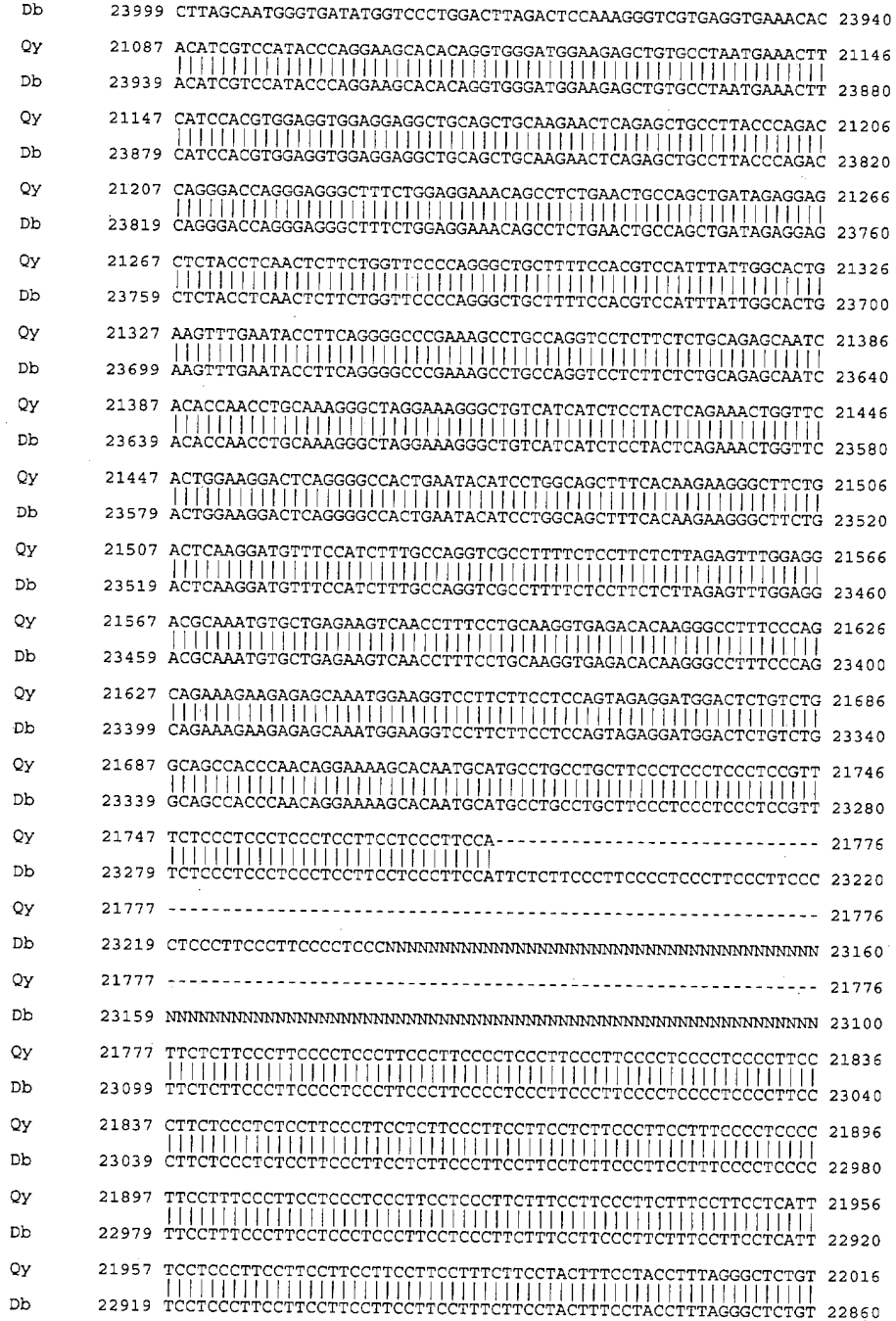
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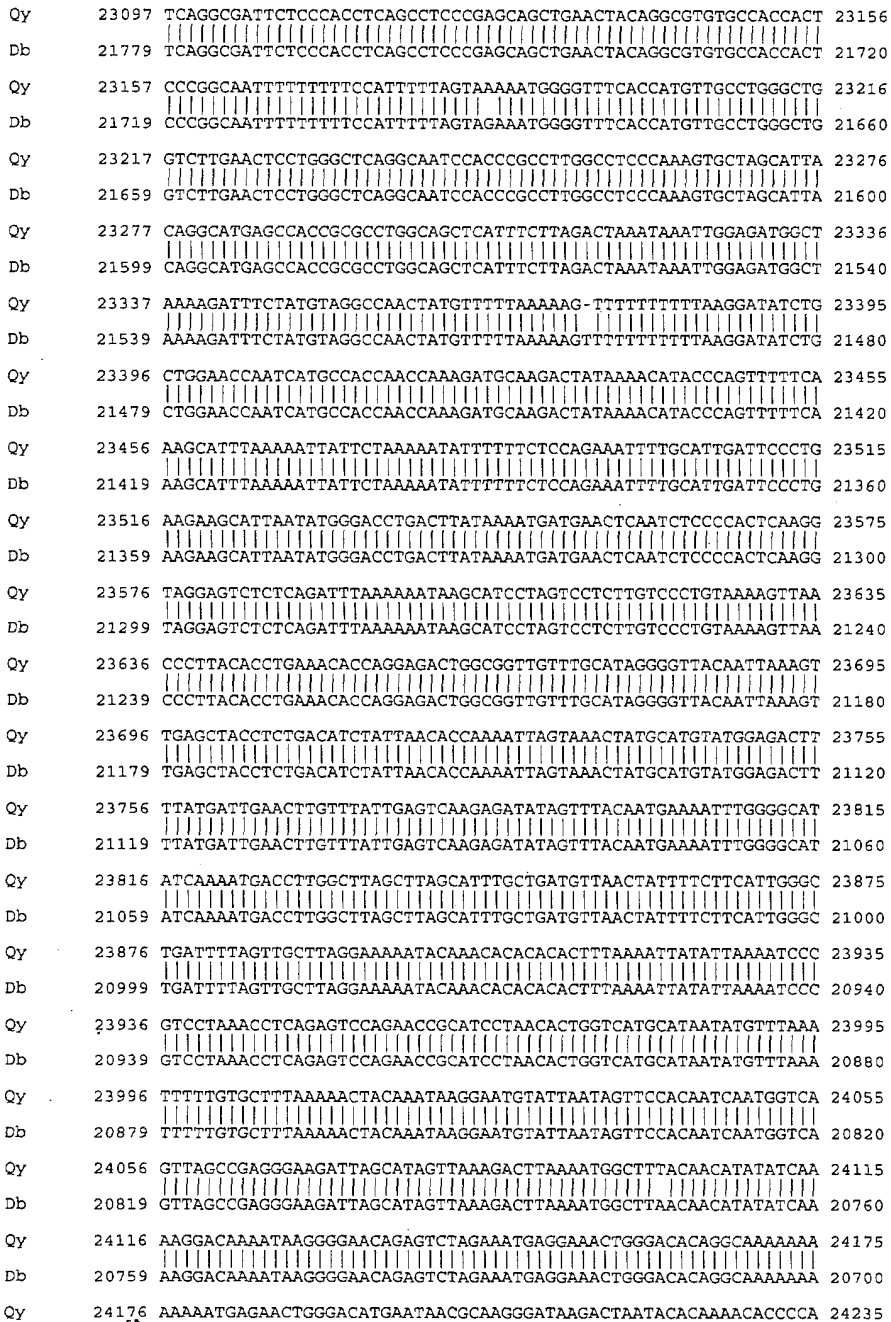
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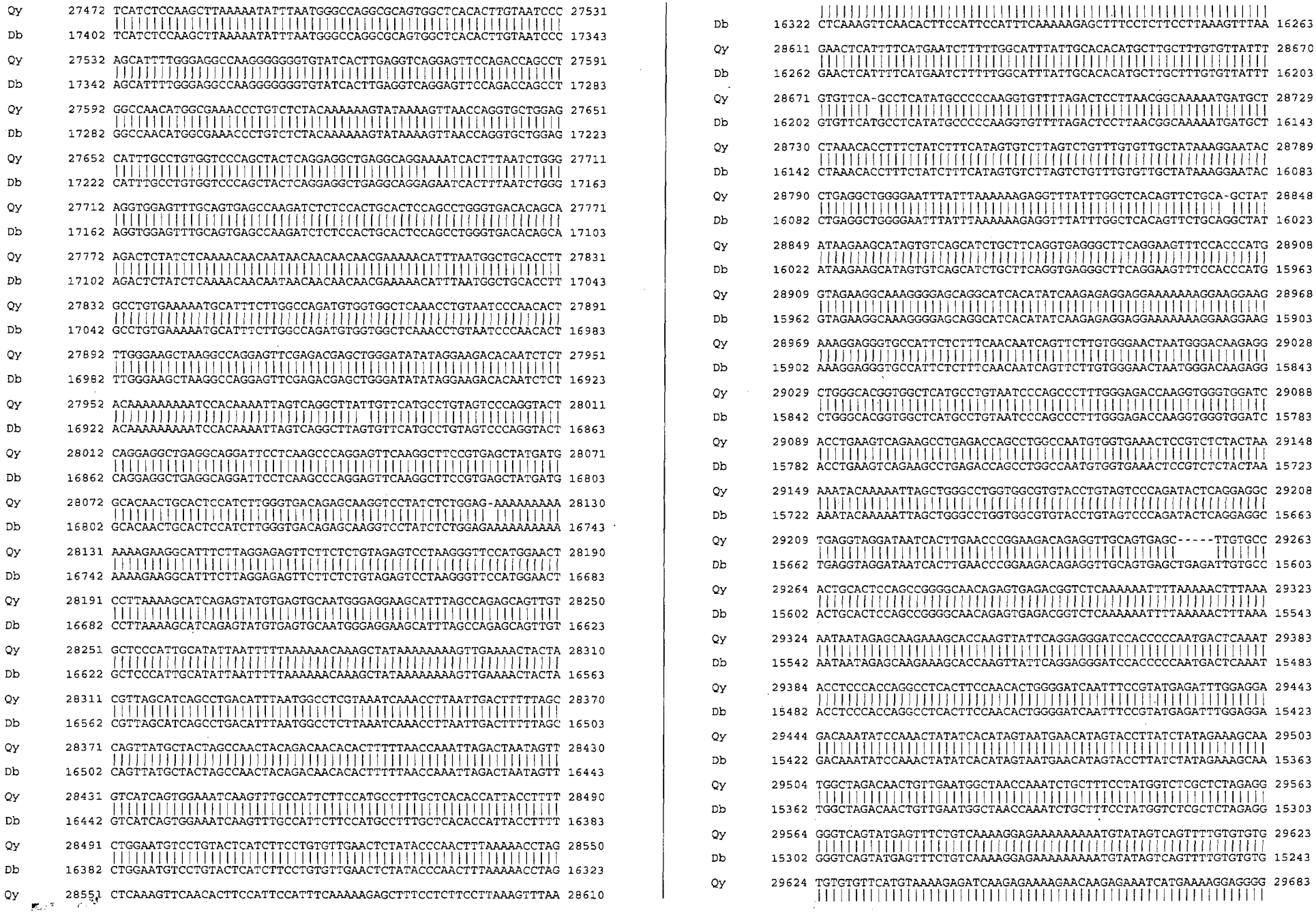

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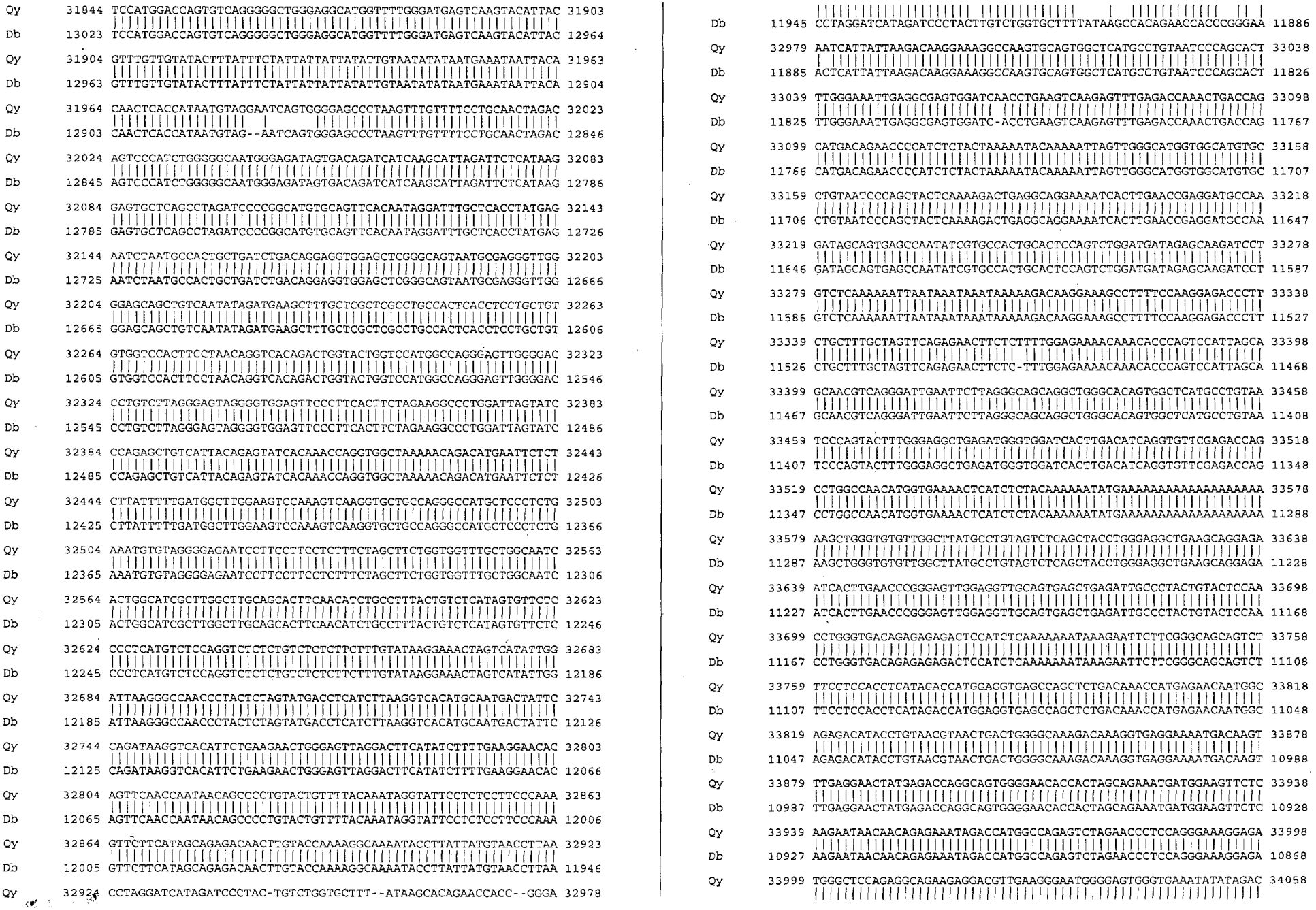
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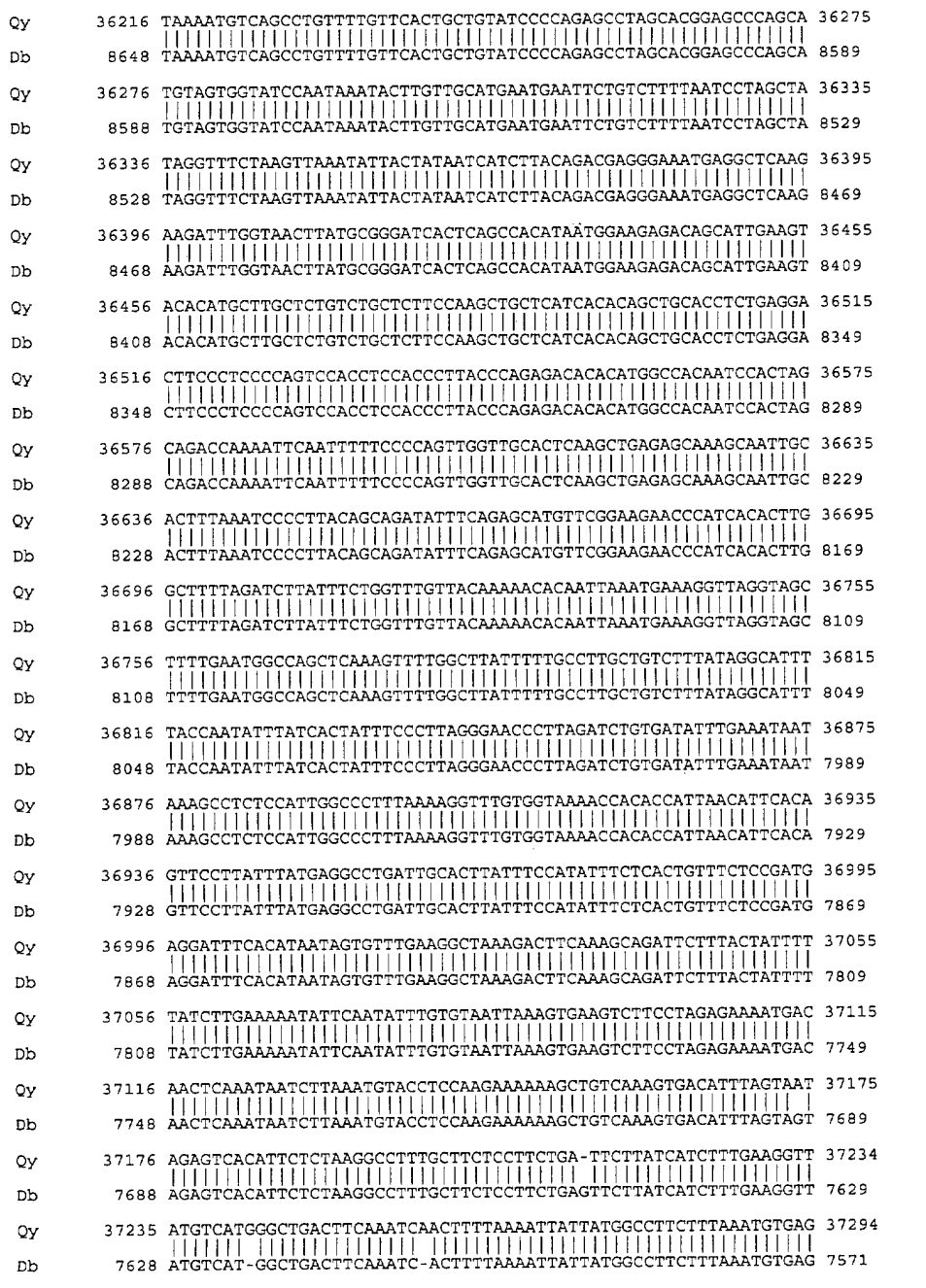
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              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      10567 GGGTGGAAGTGGCAGAG-AAGAGGGGTTTGAGCAGAGAGTGGTGATTTTTCTAATGCAGA 10509
Qy      34359 GTTGTGGGAGGTGGAGTGCAGGGAGCCAGGCTGGGTGGCTGTGCTGATGTGATTAAGCAC 34418
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Db      10508 GTTGTGGGAGGTGGAGTGCAGGGAGCCAGGCTGGGTGGCTGTGCTGATGTGATTAAGCAC 10449
Qy      34419 TTACTGACTGCCAGGCAATGGGCTAAGTACCTGAGATGCTTTGTCTGTTATCCCTCCCGA 34478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10448 TTACTGACTGCCAGGCAATGGGCTAAGTACCTGAGATGCTTTGTCTGTTATCCCTCCCGA 10389
Qy      34479 AACCCCTCTGA-GCAGGTGCAGTTATTATTCTCACTTCACAGATAAGGAAATTGAGGCAC 34537
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Db      10388 AACCCCTCTGAGGCAGGTGCAGTTATTATTCTCACTTCACAGATAAGGAAATTGAGGCAC 10329
Qy      34538 AGAGAA-TTGAGTAACTTACCCAAGGTGACATAGCTCATATATGGTAAAGCAGGCTTTGA 34596
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10328 AGAGAAGTTGAGTAACTTACCCAAGGTGACATAGCTCATATATGGTAAAGCAGGCTTTGA 10269
Qy      34597 ACTCAGTCTAGCTCCCGAACCTAAGCTTGTAACTACTATGCTTTTCCCAAAAAAAGGGGG 34656
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      34657 CTGGCACAAAAAGAGCTGA-GGGGGCTGGGCATGGTGGCTCATGCCTGTAATCCCAGCAC 34715
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      10208 CTGGCACAAAAAGAGCTGAGGGGGGCTGGGCATGGTGGCTCATGCCTGTAATCCCAGCAC 10149
Qy      34716 TTCGGGAGACTGAGGCAGGTGGTTCACCAGAGTTCAGGAGTTCGAGACCAGCCTGGTCAA 34775
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      10148 TTCGGGAGACTGAGGCAGGTGGTTCACCAGAGGTCAGGAGTTCGAGACCAGCCTGGTCAA 10089
Qy      34776 CATGGTGAAGCCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGTGGTGTGCAC 34835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10088 CATGGTGAAGCCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGTGGTGTGCAC 10029
Qy      34836 CTGTAGTCCCAGCTACTTTGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCCAGAGGCGG 34895
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      34896 ATGTTGTAGTGAGCCAAGATCATGCCACTGGACTCCAGCCTGGGTGACAGAGTGAGACTC 34955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      34956 CATCCAAAAAAAAAGAAGAGCTGAGGTGATGGCCACCATCAGCATCAGCCTGGAAGTTATA 35015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9908 CATCCAAAAAAAAAGAAGAGCTGAGGTGATGGCCACCATCAGCATCAGCCTGGAAGTTATA 9849
Qy      35016 GCAGGATGCTAAGTTTCTCTAAAGCTGTCTTTCTTAGGACTTGAAAAAGATAACTTGGGT 35075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9848 GCAGGATGCTAAGTTTCTCTAAAGCTGTCTTTCTTAGGACTTGAAAAAGATAACTTGGGT 9789
Qy      35076 TTGTATCCCATCTCTGCCATTAGTAGTTTACTGGCTTTGGATAAATTACTTAGCCTTACT 35135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      35136 GAACCAACTTTGGATTTTTATAGAGATACTGTAATGAAAGGAATAAGGTATCAGTCTTAG 35195
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Db       9728 GAACCAACTTTGGATTTTTATAGAGATACTGTAATGAAAGGAATAAGGTATCAGTCTTAG 9669
Qy      35196 CAGAGCATCCAGAGTGTTCCTATTAAAACCTAAATCATATCCTGTCATTGCTGTGCCCCA 35255
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9668 CAGAGCATCCAGAGTGTTCCTATTAAAACCTAAATCATATCCTGTCATTGCTCTGCCCCA 9609
Qy      35256 AACCATTCAATGGCTTCCCAACTCAAAGTTAAAAACTCATCTTTCCAGTGGCCTGCAAGA 35315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9608 AACCATTCAATGGCTTCCCAACTCAAAGTTAAAAACTCATCTTTCCAGTGGCCTGCAAGA 9549
Qy      35316 GCCTATGCTATCCGGTGTCTGACCTCATCTGTTGTTCCTTTCTCCCTCCCTTTCTTGGCT 35375
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Qy      35376 CCAGACGCACTCTGGTCTCCTTGCTGTTCCTTGAATACACCAGGCACACTCTCTTCGCCT 35435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9488 CCAGACGCACTCTGGTCTCCTTGCTGTTCCTTGAATACACCAGGCACACTCTCTTCGCCT 9429
Qy      35436 GAAACACTTTACCCCAGATATCTTAGCTTACTCTCTGCCTCCCTCAATTCATTGATGAAA 35495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      35496 TGTCTCAGTGAAGTCTTCTCTCTCTCCTCTGTAAAAGTATACTCTCTGTTCCCCTTCTTT 35555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9368 TGTCTCAGTGAAGTCTTCTCTCTCTCCTCTGTAAAAGTATACTCTCTGTTCCCCTTCTTT 9309
Qy      35556 ACTGTTCTAGCTACTATTGCTGTGTAACAAATCACTCCCCAAATTTAATGAGTGAAAACA 35615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9308 ACTGTTCTAGCTACTATTGCTGTGTAACAAATCACTCCCCAAATTTAATGAGTGAAAACA 9249
Qy      35616 TCAGCCATCATCTTATTTCTCACGGTTTCTGAGGGTCAGGAATTCTGGAAGGGCTCAGCT 35675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9248 TCAGCCATCATCTTATTTCTCACGGTTTCTGAGGGTCAGGAATTCTGGAAGGGCTCAGCT 9189
Qy      35676 GGGAGGTTCTGGCTCTATAATCTCTTATGCAGTGAGAGTCAGATGCTGGCTAAAACTGAA 35735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9188 GGGAGGTTCTGGCTCTATAATCTCTTATGCAGTGAGAGTCAGATGCTGGCTAAAACTGAA 9129
Qy      35736 ACAAAGCAGGGTTCTAGTAGCTGAGGGCTGGCTGGGTCTCTCAGATATAGTTCAGATCTC 35795
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9128 ACAAAGCAGGGTTCTAGTAGCTGAGGGCTGGCTGGGTCTCTCAGATATAGTTCAGATCTC 9069
Qy      35796 CTCCAGGGGGTCTCTCCACGTGGGCTAGTCTGAACTTCCTCACAGCATGGTGGCCTCAGG 35855
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9068 CTCCAGGGGGTCTCTCCACGTGGGCTAGTCTGAACTTCCTCACAGCATGGTGGCCTCAGG 9009
Qy      35856 GCAGTGGACTCTGCATAGTGGCTGAAGGCTTCGCAGCTGAGTATTCCAGCAAGCAAAGTG 35915
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Db       9008 GCAGTGGACTCTGCATAGTGGCTGAAGGCTTCGCAGCTGAGTATTCCAGCAAGCAAAGTG 8949
Qy      35916 GGAGCTGTATTGCCTCATATGACCCAACCTTGGAATCCACACAGCATCACTTCCGTGTAT 35975
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Db       8948 GGAGCTGTATTGCCTCATATGACCCAACCTTGGAATCCACACAGCATCACTTCCGTGTAT 8889
Qy      35976 TCTACGGGTTGAAAAGTCACAAAAACCAACCAGTTTCAAGGAGAAGGAACAGAGATCACA 36035
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Db       8888 TCTACGGGTTGAAAAGTCACAAAAACCAACCAGTTTCAAGGAGAAGGAACAGAGATCACA 8829
Qy      36036 TTTCTCAATTGGAGAAGGGTCAAAGTCACATTGTAATCAGAGCCTATGGGATACGAAGTA 36095
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Db       8828 TTTCTCAATTGGAGAAGGGTCAAAGTCACATTGTAATCAGAGCCTATGGGATACGAAGTA 8769
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Db       8768 TTGCGGTCAGGTATGAAAAATTTGATTTGCTGCATCTGCTTTACTTTCTCCACAGCGTTC 8709
Qy      36156 ATGATCTGCTTCTCACATGATATTGACTTACGTCATTTCTGCGTTTCCTGTCTTCCACAC 36215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8708 ATGATCTGCTTCTCACATGATATTGACTTACGTCATTTCTGCATTTCCTGTCTTCCACAC 8649
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Qy 36216 TAAAATGTCAGCCTGTTTTGTTCACTGCTGTATCCCCAGAGCCTAGCACGGAGCCCAGCA 36275
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Qy 38195 CATTTTTTGCAATTAAACACAGGAATACATAAATAAAATGCATCAGTATTTTTTACAAAT 38254
Db 6671 CATTTTTTGCAATTAAACACAGGAATACATAAATAAAATGCATCAGTATTTTTTACAAAT 6612
Qy 38255 AGCTACTAAGAGCTACTAGAAAACCTGGGAATTCTTAAAACCTTACCATGCTACTTGCTC 38314
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Qy 38315 TAAAATATTTTATTTTATGTTATTTTGTACATTTCTTTACCTACACAAACACCACTGTTT 38374
Db 6551 TAAAATATTTTATTTTATGTTATTTTGTACATTTCTTTACCTACACAAACACCACTGTTT 6492
Qy 38375 TCTTCATTTCTTAGTCTATTTAAACCTCACACCCTTTCAGCATCTCTTAATTATTTACTA 38434

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Db       6491 TCTTCATTTCTTAGTCTATTTAAACCTCACACCCTTTCAGCATCTCTTAATTATTTACTA 6432

Qy      38435 CCATCTGTTAGTTCTCCTGTCCTGAATGAAACAAAAATGGCAGAATGTAAAACGAGGGCG 38494
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Db       6431 CCATCTGTTAGTTCTCCTGTCCTGAATGAAACAAAAATGGCAGAATGTAAAACGAGGGCG 6372

Qy      38495 AACAGATTTTTGACAGGAAGTATTCAGAGGTAGAAGGAAATAGTCAAGACACATATGATA 38554
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Db       6371 AACAGATTTTTGACAGGAAGTATTCAGAGGTAGAAGGAAATAGTCAAGACACATATGATA 6312

Qy      38555 AACGAAAACAATAATAACTTTATACATAACAACTTATAGACACATTTAAAAAGTTTAAGA 38614
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Db       6311 AACGAAAACAATAATAACTTTATACATAACAACTTATAGACACATTTAAAAAGTTTAAGA 6252

Qy      38615 TCTCAAGAGCTATGTCTGAATAGATAGGAGTAAAAACTCTATTAAGTAATTAGGAAAATA 38674
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Qy      38675 ACAAGAACAGTGAATTTCTTAATGAATGGCATGTAATCAAAACTGTACTTATCGTCTAAT 38734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6191 ACAAGAACAGTGAATTTCTTAATGAATGGCATGTAATCAAAACTGTACTTATCGTCTAAT 6132

Qy      38735 TCATAATCTTGAATGTTTTTATTTTATTTATTTATTTTTTTATTTTTTGAGACAGAGTCT 38794
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Qy      38795 TGCTCTGTCACCCAGGCTAGAGTACAGTGGCGTGATCTCAGCTCACTGCAACCTCCACCT 38854
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Db       6071 TGCTCTGTCACCCAGGCTAGAGTACAGTGGCGTGATCTCAGCTCACTGCAACCTCCACCT 6012

Qy      38855 CCCAGGTTCAAGCGATTCTGCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGAGGCCTG 38914
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Db       6011 CCCAGGTTCAAGCGATTCTGCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGAGGCCTG 5952

Qy      38915 CCACTGCACCCGGCTAATTTCTGTATTTTTAGTAGAGATGGGGTTTCACCATCTTGGCCA 38974
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Db       5951 CCACTGCACCCGGCTAATTTCTGTATTTTTAGTAGAGATGGGGTTTCACCATCTTGGCCA 5892

Qy      38975 GGCTGGTCTTGAACTCCTGACCTCATGATCCACCAGCCTTGGCCTCCCAAAGTGCTGGGA 39034
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Db       5891 GGCTGGTCTTGAACTCCTGACCTCATGATCCACCAGCCTTGGCCTCCCAAAGTGCTGGGA 5832

Qy      39035 TTACAGGCGTGAGCCACCACGCCTGGTCGAATGTCTTTATTATTTGAAGAGACAACATGG 39094
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Qy      39095 GCCTTAAATCTGTCTTCTATTTGACAGACTTTGATGGAGTCAAATCCCAATGCTGCCACT 39154
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Db       5771 GCCTTAAATCTGTCTTCTATTTGACAGACTTTGATGGAGTCAAATCCCAATGCTGCCACT 5712

Qy      39155 TACTGAACGGCCTTAAATGACTTAGTCTCTCTCAGCTGTCTTTCTGCATATGTAAGGTGG 39214
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Qy      39215 AATAATGATGGCTTTCAAGGAGGAATAAACCTATGAAAAGTGTTGAGGATAGTGTTTGAT 39274
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Db       5651 AATAATGATGGC-TTCAAGGAGGAATAAACCTATGAAAAGTGTTGAGGATAGTGTCTGAT 5593

Qy      39275 ATGAAATAAGGATTTCAACAAGTAGTAGCTGCTATTGAAGATTTAAGAGTTATTTATTAC 39334
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Db       5592 ATGAAATAAGGA-TTCAACAAGTAGTAGCTGCTATTGAAGATTTAAGAGTTATTTATTAC 5534

Qy      39335 AACTATTTAATAAAATTTTAAAAACTAATACACTTAAATTATTAAAGAGCTTTGAAATGG 39394
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Db       5533 AACTATTTAATAAAATTTTAAAAACTAATACACTTAAATTATTAAAGAGCTTTGAAATGG 5474

Qy      39395 GCCAGGCGCAGTAGCTCCTGCCTGTAATCCCAACACTTTGGGAGGCCAAGGTGGGCGGAT 39454
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Db       5473 GCCAGGCGCAGTAGCTCCTGCCTGTAATCCCAACACTTTGGGAGGCCAAGGTGGGCGGAT 5414

Qy      39455 CACCTGAGGTCAGGAGTTTAAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTA 39514
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Db       5413 CACCTGAGGTCAGGAGTTTAAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTA 5354

Qy      39515 AAAACGCAAAAATTAGCCAGGTGTGGTGGCATGCACCTGTAGTCCCAACTACTCAGGAGG 39574
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Db       5353 AAAACGCAAAAATTAGCCAGGTGTGGTGGCATGCACCTGTAGTCCCAACTACTCAGGAGG 5294

Qy      39575 TTGAGGGAGGAGAATTGCTTGAACCTAGGAGGTGGAGGTTGCAGTAACCCGAGATGTCAC 39634
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       5293 TTGAGGGAGGAGAATTGCTTGAACCTAGGAGGTGGAGGTTGCAGTGACCCGAGATGTCAC 5234

Qy      39635 TGCACTCCAGCCTGGCAACAGAGCAAGACTCCATAAAGACAACAAAAGCTTTGAAATTGT 39694
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Db       5233 TGCACTCCAGCCTGGCAACAGAGCAAGACTCCATAAAGACAACAAAAGCTTTGAAATTGT 5174

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Qy      39755 GACATGAGAGCTTCCAGCAATTTTTAATTAAGCCCTCACAGATTTTATGTCACTGGCTAT 39814
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Qy      39815 GTGATAAACAAATTATTTGCTAAAATAATATTCTTGCTTCTTTTTTAAGGAATTGTCTCC 39874
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Qy      39875 CTAGAAACGGTTTGTACCAAACAATACACTGACTTTACACAAAATCAGATCTGATTGGCA 39934
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Qy      39935 ACAGTTGCAGATGTTTTCAAAAGATTTTCATTTGAGAAGGGGCCCATTTGGGTTATTTAG 39994
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Qy      39995 ATTCTA 40000
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RESULT 9
U82209
LOCUS       U82209                 11841 bp    DNA     linear   HTG 30-AUG-2001
DEFINITION  Homo sapiens chromosome 10 clone CRI-JC2012 map 10q22.3.
ACCESSION   U82209
VERSION     U82209.1  GI:3983515
KEYWORDS    HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11841)
  AUTHORS   Smith,D.R.
  TITLE     Sequencing of Human Chromosome 10
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 11841)
  AUTHORS   Du,L. and Smith,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-DEC-1996) Bioinformatics Division, Genome
            Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA
COMMENT     On Dec 9, 1998 this sequence version replaced gi:1773047.
            Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing
            Technology. Data may contain low quality seq uence and BAC/Cosmid
            vector sequences.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *         1    11841: contig of 11841 bp in length.
FEATURES              Location/Qualifiers
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                     /clone="CRI-JC2012"
ORIGIN

  Query Match             13.6%;  Score 5429.6;  DB 2;  Length 11841;
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Qy       3347 GATCACCATAACAGATATAAGAATCATGGCAAAGTTTGAAATATTCTTGAGAATTAGCAA 3406
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Db       1954 GATCACCATAACAGATATAAGAATCATGGAAAAGTTTGAAATATT-TTGAGAATTAGCAA 2012

Qy       3407 AGTGTGACACAGAGAAACAAAGTGAGCACATGCCGTTGGAAAAAATTGGTGTTGATAGAC 3466
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Qy       3467 TTGCTCCATCGCAAGTTTGCCATACGCCTTCAATTTATAAAAAACACAATATCTAGGAAG 3526
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Db       2073 TTGCTCCAT-GTAAGTTTGCCATACGCCTTCAATTTATAAAAAACACAATATCTAGGAAG 2131

Qy       3527 TTCAATAAAGTGAAGTGCAATAAGATGAAGTATGCCTGTAAATATTTCAGGCTTTCCAGA 3586
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Qy       3587 CCATAGGGTTTCTGTTGCAACTGCTCACCTCTGCCATTATAGCATGAAAGCAGCTATAGA 3646
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Qy       3707 CTTGAGGTCAGGAATTCGAGACCAGCTTGGCCAACATGGCAAAACCCCGTCTCTACTAAA 3766
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Qy       3767 AATACAAAAATGAGCCAGGACTACGCATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGG 3826
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Qy       3827 CAGGAGAATCTCTTGAACCCGGGAAGGGGAGGTTACAGTGAGCCAAGATTGTGCCACTGC 3886
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Qy       4186 AATGCATTATGCAATTCATTGCTATTAGACCTGTGCTATAAAATAGCAATGAATTATGTC 4245
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Qy       4246 AGTTTTTATTTGTCTGAAAAAGTTTTTTGTTTTTGAAATATACTTTTGCTGGGTATATAA 4305
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Qy       4426 GTTTGATGTGTCTAGGAGTGATTTTCTTTGTATTTATCCTTTTGGGGGGCCTCTTAATTTC 4485
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Qy       4544 TGGGCTGAAAAAAAAAGAAAAATAAAATCATAGTTTAAAAAACTAATTTTGGAAAATTTT 4603
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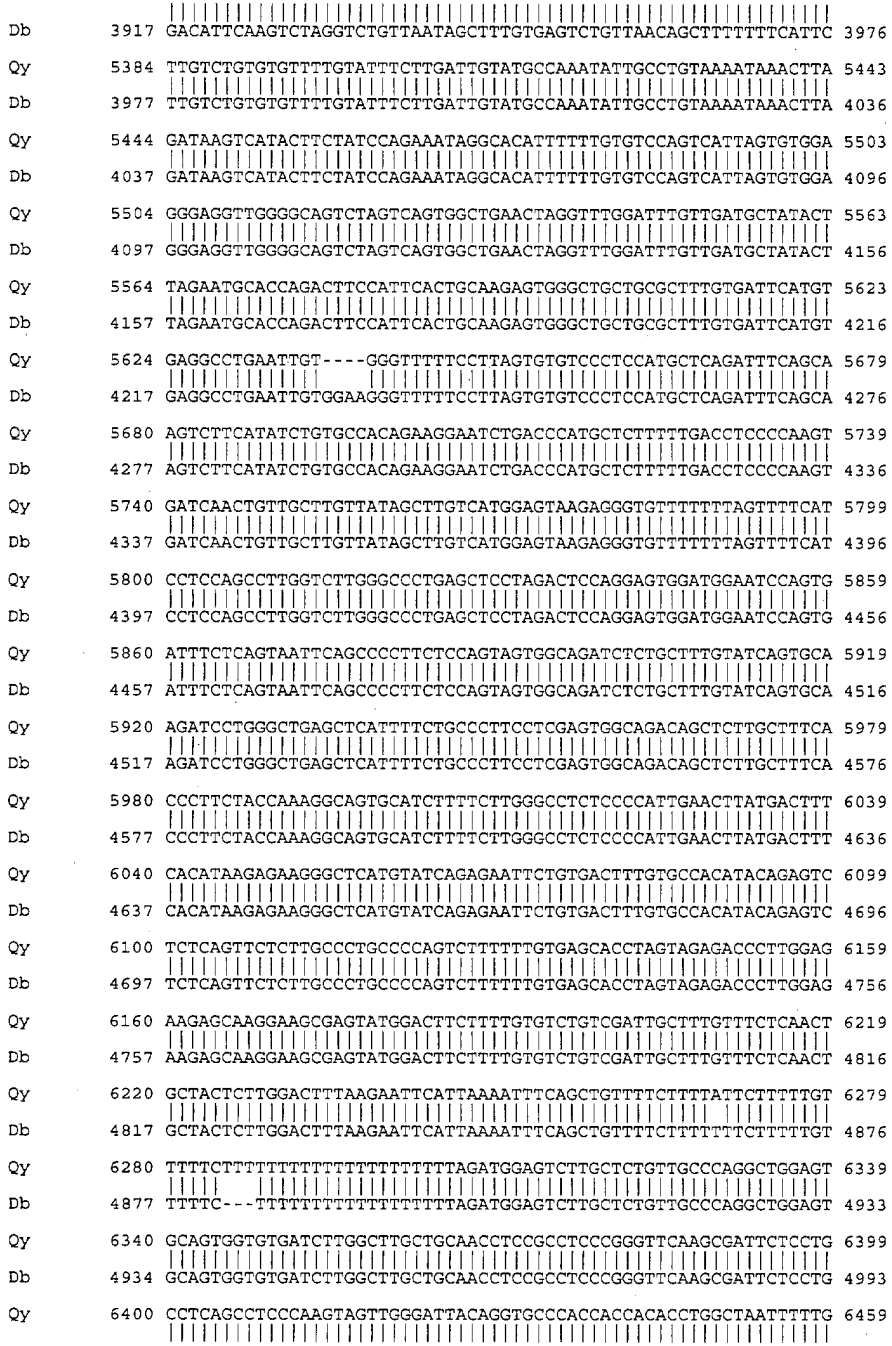
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Db       6248 AGTTTTCAAATATTCATAAGTACCTACTGTGCAGGGAAAGAACATGCCATACAAAAGATG 6307

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Db       6368 GGGAAGTAGCAGTATGGTACAAGATAATACATACATATCAGTGAATGATATTGCCAAAAA 6427

Qy       7839 GTGCTATTGATAGAGAAATAATTCATTTCTGCAAACAGCTGCTGATCTCCTACTGAAAAC 7898
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       6428 GTGCTATTGATAGAGCAATAATTCATTTCTGCAAACAGCTGCTGATCTCCTACTGAAAAC 6487

Qy       7899 AGAGGAGGGAGAACAGGACGCCTCGTGGTCAGGATAGAAGAGAAAGACCTTGAGTTGAGC 7958
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Db       6488 AGAGGAGGGAGAACAGGACGCCTCGTGGTCAGGATAGAAGAGAAAGACCTTGAGTTGAGC 6547

Qy       7959 CTTGAACAGTATTTAATATTCAAAAGGTTAAGAGAGGAGAGCAATTGAGGAGGGGAGAAT 8018
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Db       6548 CTTGAACAGTATTTAATATTCAAAAGGTTAAGAGAGGAGAGCAATTGAGGAGGGGAGAAT 6607

Qy       8019 AGTTCCAGCACAAATGATGGTGTACAAGATGAACACAGTCAGTAAAGAGCAGACTGGTCT 8078
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Db       6608 AGTTCCAGCACAAATGATGGTGTACAAGATGAACACAGTCAGTAAAGAGCAGACTGGTCT 6667

Qy       8079 GGATGGAGAGGAGGATTTGCATCATTTGGGATTACGTCATTTAGACCCTTGAAAGCCAGG 8138
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Db       6668 GGATGGAGAGGAGGATTTGCATCATTTGGGATTACATCATTTAGACCCTTGAAAGCCAGG 6727

Qy       8139 ATTGAGTAAAGCCACAGTGAAGCGACTGGCTCGTATGGAAGCTTTATTTTAAGAAGATTA 8198
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Qy       8199 ATCTGGTAGTGACATGTGCCAAAAACTGAATAGGTAGAAATGAGATGCAGAGAGCCCAGT 8258
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Db       6788 ATCTGGTAGTGACATGTGCCAAAAACTGAATAGGTAGAAATGAGATGCAGAGAGCCCAGT 6847

Qy       8259 TAGAACTAAGTCTGGTGCAGTAATGCAGGATTGAGGCAATAAACACCAAACTACAGTATC 8318
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Qy       8319 ACCAGATAATGGATGTTTGAACGGACGGTTTAAAGGAAAATTGATGGTATTTGGTAATTT 8378
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Qy       8379 ATTAGATAATCCAGGGCCATGGAATGAGAGGGGAAAATGACTAACCATAGTCATCAAATG 8438
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Qy       8499 TTGGTACAGCTGACTATGATAATGACTGCTACCATGCTTGTTCCTCTTTTAGCAGCTGTG 8558
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Db       7088 TTGGTACAGCTGACTATGATAATGACTGCTACCATGCTTGTTCCTCTTTTAGCAGCTGTG 7147

Qy       8559 AGTCCCCCACCAGCCAAACAATGAGCCTCTTGAAAAGGACGATGCCTTTTCACTTCTCTC 8618
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Db       7148 AGTCCCCCACCAGCCAAACAATGAGCCTCTTGAAAAGGACGATGCCTTTTCACTTCTCTC 7207
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Qy       8619 CAAGTGCTTGGCAAATAGGAGGCCTTTTGAAGTTACTTTATAGTTAGGGGTTCCCAGTGA 8678
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Db       7208 CAAGTGCTTGGCAAATAGGAGGCCTTTTGAAGTTACTTTATAGTTAGGGGTTCCCAGTGA 7267

Qy       8679 GTATTTGAAATATTAAGTCATGCCCGTGGTTGACAGCATGGCCCTACTGCTCATCATCAG 8738
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Qy       8739 CTATTAACCTTAGGCAAGTTAATGAACTTTTCTAAGCCCCAGTCTACTCATTTATAAAGT 8798
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Db       7328 CTATTAACCTTAGGCAAGTTAATGAACTTTTCTAAGCCCCAGTCTACTCATTTATAAAGT 7387

Qy       8799 GGGATTATTAATAATGTCTACTTCATAAAATTATGAAGCCTGAGTTAGGTCATTCAGATA 8858
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Db       7388 GGGATTATTAATAATGTCTACTTCATAAAATTATGAAGCCTGAGTTAGGTCATTCAGATA 7447

Qy       8859 GTGTTTAGTCTGATTCTTCGAACCTAGTAAACAGTCAGTAAACAGAAGCAAATGCCACAT 8918
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Db       7448 GTGTTTAGTCTGATTCTTCGAACCTAGTAAACAGTCAGTAAACAGAAGCAAATGCCACAT 7507

Qy       8919 GCCTGATTTATATCCAAGGGGAGAAAGGTAAA 8950
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RESULT 10
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LOCUS       HSU49973                2418 bp    DNA     linear   PRI 28-JUN-1997
DEFINITION  Human Tigger1 transposable element, complete consensus sequence.
ACCESSION   U49973
VERSION     U49973.1  GI:2226003
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2418)
  AUTHORS   Smit,A.F. and Riggs,A.D.
  TITLE     Tiggers and DNA transposon fossils in the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 93 (4), 1443-1448 (1996)
  MEDLINE   96202298
   PUBMED   8643651
REFERENCE   2  (bases 1 to 2418)
  AUTHORS   Robertson,H.M.
  TITLE     Members of the pogo superfamily of DNA-mediated transposons in the
            human genome
  JOURNAL   Mol. Gen. Genet. 252 (6), 761-766 (1996)
  MEDLINE   97074895
   PUBMED   8917322
REFERENCE   3  (bases 1 to 2418)
  AUTHORS   Robertson,H.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-1996) Hugh M. Robertson, Entomology, University
            of Illinois at Urbana-Champaign, 505 S. Goodwin, Urbana, IL 61801,
            USA
COMMENT     On Jun 28, 1997 this sequence version replaced gi:1224064.
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ORIGIN

  Query Match             3.7%;  Score 1471.6;  DB 9;  Length 2418;
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  Matches 2080;  Conservative    0;  Mismatches  304;  Indels  236;  Gaps   19;

Qy        979 CAGGCATACCTTGGAGATACTGTGGGTTTGGTTCCATACCACCACAATAATACAAATATG 1038
              |||||||||||  ||||||  ||  |||||  |||||||  ||||||  ||||||   |||
Db       2418 CAGGCATACCTCGGAGATATTGCGGGTTCGGTTCCAGACCACCGCAATAAAGCAA----- 2364

Qy       1039 CAAGAAGTGGATATCACAATAAAGTGAGTCACACAAGTCTTTTGGCTTCCCAGTGCATAT 1098
                  |||||  ||||||||  |||||||||  | |  ||||||  ||||||||||||||
Db       2363 ----------ATATCGCAATAAAGCGAGTCACACGAATTTTTTGGTTTCCCAGTGCATAT 2314

Qy       1099 AAAAGTTTTGCTTATACTACACTGTAGTCTGTTAAGTGTGCAATAGTGTTATGTCTAAAA 1158
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Db       2313 AAAAGTTATGTTTACACTATACTGTAGTCTATTAAGTGTGCAATAGCATTATGTCTAAAA 2254

Qy       1159 AA----ACACATACCTTAATTTTAAAATGCTTTATTACTAAAAAATGCTAACAATCATTT 1214
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Db       2253 AACAATGTACATACCTTAATTTAAAAATACTTTATTGCTAAAAAATGCTAACGATCATCT 2194

Qy       1215 GAGCATTCAGTGAGTTGTAATCTTTTTGCTGGTGGAAGGTCTTTTCTTATTGATGACTGA 1274
              ||||  |||||  ||||  ||||||||||||||||||||  ||||||    ||  |||  |
Db       2193 GAGCCTTCAGCGAGTCGTAATCTTTTTGCTGGTGGAGGGTCTTGCCTCGATGTTGATGGC 2134

Qy       1275 T-----------CGGGGGTCAGGTGCTGAAGCTTAGGGTGGCTGTGGCAGTTTCTTAAA- 1322
              |           |||  |   | ||||||||  || ||||||||||||||  |||||||||
Db       2133 TGCTGACTGATCAGGGTGGTGGTTGCTGAAGGTTGGGGTGGCTGTGGCAATTTCTTAAAA 2074

Qy       1323 ----ACAACAGTGAAGATTGCAATATCAGTTGACTCTTCCTTTCATGAAAGATTTCTCTC 1378
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Db       2073 TAAGACAACAATGAAGTTTGCCGCATCGATTGACTCTTCCTTTCACGAAAGATTTCTCTG 2014

Qy       1379 TAGTGTGTGATGCTTTTTGATAGCATTTTATGCACAGTAGAACTTCTTTGAAAATTGGA- 1437
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Db       2013 TAGCATGCGATGCTGTTTGATAGCATTTTACCCACAGTAGAACTTCTTTCAAAATTGGAG 1954

Qy       1438 TCAATCCTCTCAAACCCTGCTCTGCTTTAACAACCTAAGTTAATATAATATTCTGAATCC 1497
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Db       1953 TCAATCCTCTCAAACCCTGCCGCTGCTTTATCAACTAAGTTTATGTAATATTCTAAATCC 1894

Qy       1498 ATTGTTGTCATTTCAACAATTTTCACAGTGTCTTCACCAGGAGTAGATTCCATCTCATTT 1557
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Db       1893 TTTGTTGTCATTTCAACAATGTTCACAGCATCTTCACCAGGAGTAGATTCCATCTCAAGA 1834

Qy       1558 CCTGAGATGGAATCTTTGCTCATCCATAAGAAGAAATTCCTCATCTGTTCAAGTTTTATC 1617
                |  |  ||||||||||||||||||||||  ||  ||||||||  ||||||||||||||
Db       1833 AACCACTT----TCTTTGCTCATCCATAAGAAGCAACTCCTCATCCGTTCAAGTTTTATC 1778

Qy       1618 ATGAGATTGCAGCAATACAGTCATGTCTTCAGGCCTCACTTCACTTTTAATTCCAGTTCT 1677
              ||||||||||||||||  ||||||  ||||||||     ||  |||||  ||||||  ||||||
Db       1777 ATGAGATTGCAGCAATTCAGTCACATCTTCAGG-----CTCCACTTCTAATTCTAGTTCT 1723
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Qy       1678 CTTGCTGTTTCTACCACATCTGTGGTTCCTTCCTCCATTGAAGTCTTGAACCTCTCCAAG 1737
              ||||||  ||||  ||||||||||  |||  ||||||||  ||||||||||||  |||  |||
Db       1722 CTTGCTATTTCCACCACATCTGCAGTTACTTCCTCCACTGAAGTCTTGAACCCCTCAAAG 1663

Qy       1738 TCATCCATGAGGGTTGGAATCGACTTCTTCCAAATTCCTGTTAATATTTATATTTTGA-- 1795
              ||||||||||||||||||||  ||||||||||  |||||||||  ||  |||||||||
Db       1662 TCATCCATGAGGGTTGGAATCAACTTCTTCCAAACTCCTGTTAATGTTGATATTTTGACC 1603

Qy       1796 -CCTCCCATGAATCATGAATGTTCTTAATGGCACCTGGAATGGTGAATCCTTTCCAAAAG 1854
               ||||||||||||||  |||||||||||||||||||  ||  |||||||||||||||||  |||
Db       1602 TCCTCCCATGAATCACGAATGTTCTTAATGGCATCTAGAATGGTGAATCCTTTCCAGAAG 1543

Qy       1855 GTTTTCAATTTACTTAGTCCAGATCCATCCATCCAGAGGATCCACTTTCAATGCCAGTTA 1914
              ||||||||||||||  |  |||||||||      ||||||   |||  ||  |||  |||  ||
Db       1542 GTTTTCAATTTACTTTGCCCAGATCCAT-----CAGAGGAATCACTATCTATGGCAGCTA 1488

Qy       1915 TAGCCTTATGGAATGTATTTCTTCAATAATAAGGCTTGAAAGTTGAAATTACTCCTTGAT 1974
              |||||||  |  ||||||||||||  |||||||||  |||||||||  ||||||||||||||||
Db       1487 TAGCCTTACGAAATGTATTTCTTAAATAATAAGACTTGAAAGTCGAAATTACTCCTTGAT 1428

Qy       1975 CCATTTTCTGCAAAATAGATGTTGTGTTAGCAGGCATGAAAGCAACATTAATCTTTTTGT 2034
              ||||   |||||  |||  |||||||||||||||||||||||  ||||||||||||  ||||
Db       1427 CCATGGGCTGCAGAATGGATGTTGTGTTAGCAGGCATGAAAACAACATTAATCTCCTTGT 1368

Qy       2035 ACATGTCCATCAGAGCTCTTGGGTGACCAGGTATATTGCCAGTGAGCAGTAATACTTTGA 2094
              ||||  |||||||||||||||||||||||||||||||||||  ||||  ||||||||||  |||||
Db       1367 ACATCTCCATCAGAGCTCTTGGGTGACCAGGTGCATTGTCAATGAGCAGTAATATTTTGA 1308

Qy       2095 AAGGAAT-TATTTTTCTTAGCAGTAGGTCTCAACAATGGGCTTAAAATATTTGGTCCACC 2153
              |||  |||  |  |||||||  |||||||||||||||||  ||||||||||||||  ||  |||
Db       1307 AAGAAATCTTTTTTTCTGAGCAGTAGGTCTCAACAGTGGGCTTAAAATATTCAGTAAACC 1248

Qy       2154 ATTCTGTAAACTGATGTGCTGTCATCTAAACTTTGTAGTTTCATTTATAGAGCACAGGCA 2213
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Db       1247 ATGCTGTAAACAGATGTGCTGTCATCCAGGCTTTGTTGTTCCATTTATAGAGCACAGGCA 1188

Qy       2214 GAGTAGATGTAGCATAATTCTTAAGGGACTTAGGATTTTCAGAATGGTAAATGAACATTG 2273
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Db       1187 GAGTAGATTTAGCATAATTCTTAAGGGCCCTAGGATTTTCGGAATGGTAAATGAGCATTG 1128

Qy       2274 GCATCAATTTAAA-TCACTAGCTGTATTAGCCCCCAACAAGAGAGTCAGCCTATTTTTTG 2332
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Db       1127 GCTTCAACTTAAAGTCACCAGCTGCATTAGCCCCTAACAAGAGAGTCAGCCTGTCCTTTG 1068

Qy       2333 AAGCTTTGAAGCCAAGCGTCGACTTCTCCTCCCTGGTTACAAAAGTCCTAAATGGCATCT 2392
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Qy       2393 TCTTCCAATATAAGGCTGTTTTATCTACATTGAAAATCTGTTGTTTAGTGTAGCCACCTT 2452
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Db       1007 TCTTCCAATAGAAGGCTGTTTCGTCTACATTGAAAATCTGTTGTTTAGTGTAGCCACCTT 948

Qy       2453 CATCAATGATACTATCTAGATCTCTTGGATAACTTG-TGCAGCTTCTACATCAGCATTTG 2511
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Db        947 CATCAATTATCTTAGCTAGATCTTCTGGATAACTTGCTGCAGCTTCTCCATCAGCACTTG 888

Qy       2512 CTACTTCACCTTGTACTCTTATGTAATGGAGT-GGCATCTTTCCTCGTACCTCATGAACC 2570
              ||  ||||||||||  |||  ||||||  |||  ||||||||   ||||||||||||
Db        887 CTGCTTCACCTTGCACTTTTATGTTATGGAGACGGCTTCTTTCCTTAAACCTCATGAACC 828

Qy       2571 AACCTCTGCTAGCTTCCAACTTTTCTTCTGTAGTTTCCTCGCCTCTCTCAGCCTTCATAG 2630
              ||||||||||||||||||||||||||||||  ||  ||||||  ||||||||||||||||||||
Db        827 AACCTCTGCTAGCTTCCAACTTTTCTTCTGCAGCTTCCTCACCTCTCTCAGCCTTCATAG 768

Qy       2631 ACTTGAGGATAGTTAGAGACTTGCTTTGGATTAGATTTTGGCTTCAGGAAATGTTGTGGC 2690
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Db        767 AATTGAAGAGAGTTAGGGCCTTGCTCTGGATTAGGCTTTGGCTTAAGGGAATGTTGTGGC 708

Qy       2691 TGGTTTGATCTTCTATCCAGACCACTAAAACTTTATCCATATCAGCAATAAGGCTGTTTT 2750
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Db        707 TGGTTTGATCTTCTATCCAGACCACTAAAACTTTCTCCATATCAGCAATAAGGCTGTTTC 648
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Qy       2751 GCTTTCTTATTATTTGTGTGTTCACTGGAGTAGCACTTTTAATTTGCTTCAAGATATATT 2810
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Qy       2811 TCTTTGCATTCACAACTTGGCTGACTGGT----GCAAGAGGCCTAGCTTTCAGACTATCT 2866
Db        587 CCTTTGCATTCACAACTTGGCTAACTGTTTGGCGCAAGAGGCCTAGCTTTCGGCCTATCT 528

Qy       2867 TGGCTTTTGACATGCCTTCCTCACTAAGCTTAATCATTTCTAGCTTTTGATTTAAAATGA 2926
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Qy       2927 GAGATGTAGGCCAGGCACAGTGGCAGGCACAGTGGCATATGCCTGTAATTCCAACACATT 2986
Db        467 ------------------------------------------------------------ 468

Qy       2987 AAGAGGCCAAGGTGGGAGGATTGCTTGAACCCAGGAGGTGGAGGTTGTAGAGATCACACC 3046
Db        467 ------------------------------------------------------------ 468

Qy       3047 ACTGCATTCCGTCCTGGATGACAGAGCAAGACCTTTCTCAAAATAAAATGAGAGGTGTGC 3106
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Qy       3107 TTCTTCTTTTTGTTTGAGCCCATAGAAGCCATAGTATGATTTTTAATTGGCCTAATTTCA 3166
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Qy       3227 CTGGTCAGTGGAGCAGTCAGAACACACATAACACTAATAAATT--GTTTGCTGTCTTATA 3284
Db        336 CCGGTCGGTGGAGCAGTCAGAACACACACAACATTTATCGATTAAGTTCGCCGTCTTATA 277

Qy       3285 TGGATGTGGTTTGTGATGCCCCCAAACAATTACAATAGTTACAGCAAATATCACTGATCA 3344
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Qy       3345 CAGATCACCATAACAGATATAAGAATCATGGCAAAGTTTGAAATATTCTTGAGAATTAGC 3404
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Qy       3405 AAAGTGTGACACAGAGAAACAAAGTGAGCACATGCCGTTGGAAAAAATTGGTGTTGATAG 3464
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Qy       3525 AGTTCAATAAAGTGAAGTGCAATAAGATGAAGTATGCCTG 3564
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LOCUS       AC092165               100020 bp    DNA     linear   PRI 21-FEB-2002
DEFINITION  Homo sapiens BAC clone RP11-753F4 from 2, complete sequence.
ACCESSION   AC092165
VERSION     AC092165.4  GI:18056750
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100020)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
    PUBMED  9847074
REFERENCE   2  (bases 1 to 100020)
  AUTHORS   Abbott,S. and Haglund,K.
  TITLE     The sequence of Homo sapiens BAC clone RP11-753F4
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 100020)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 100020)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JAN-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 100020)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-FEB-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Jan 4, 2002 this sequence version replaced gi:17981677.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0753F04
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO. For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries. Genomics 51:1-8. The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at http://www.chori.org
            VECTOR:  pBACe3.6

            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-762N20, 2000 bp overlap;
            the clone sequenced to the right is RP11-485D7.  Actual start of
            this clone is at base position 98039 of RP11-762N20; actual end is
            at base position 100020 of RP11-753F4.

            Data from AC09338 and AC074188 was used to finish this clone,
            AC092165. Polymorphisms have been identified between AC074188 and
            AC092165.
FEATURES              Location/Qualifiers
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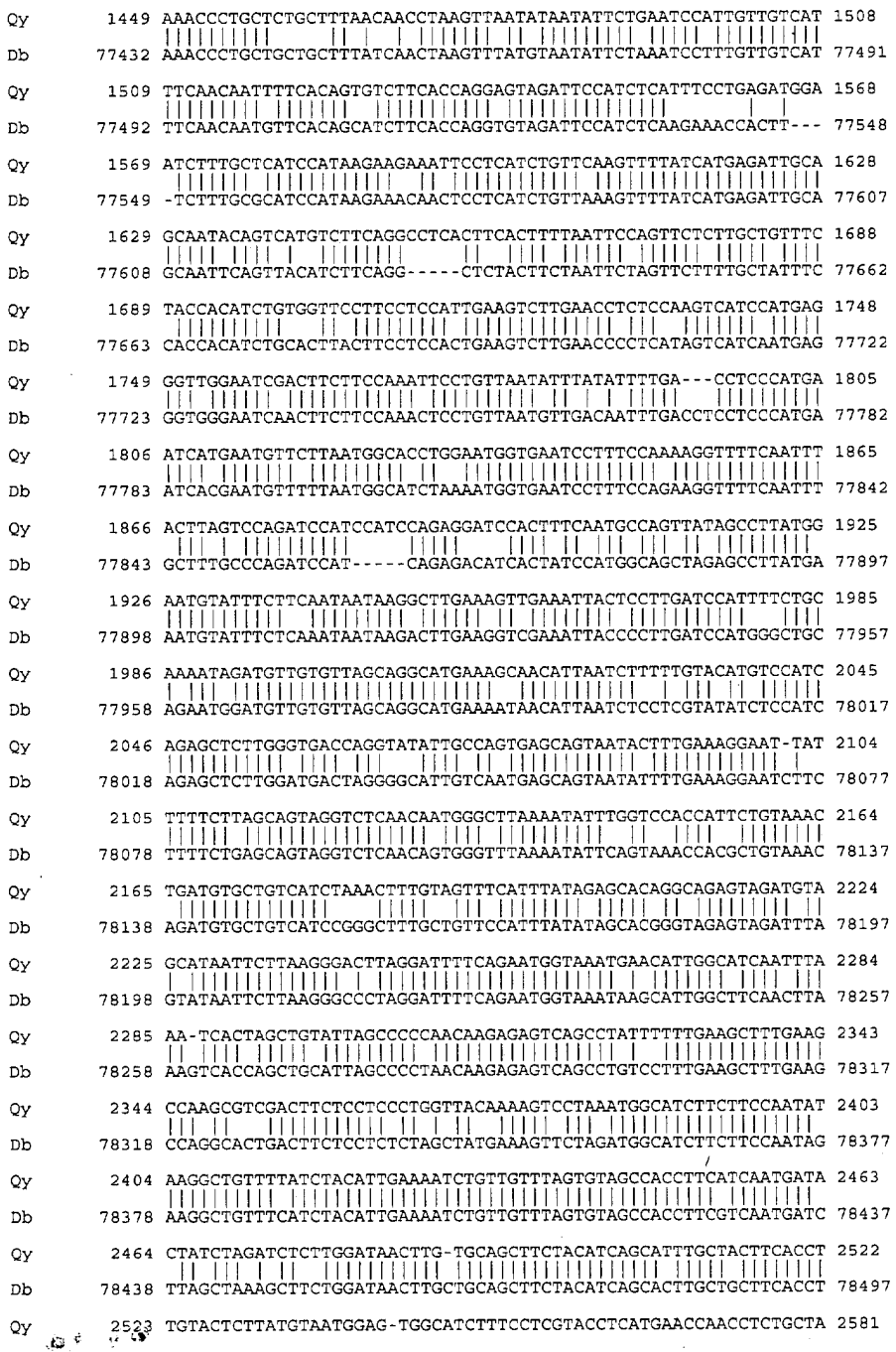
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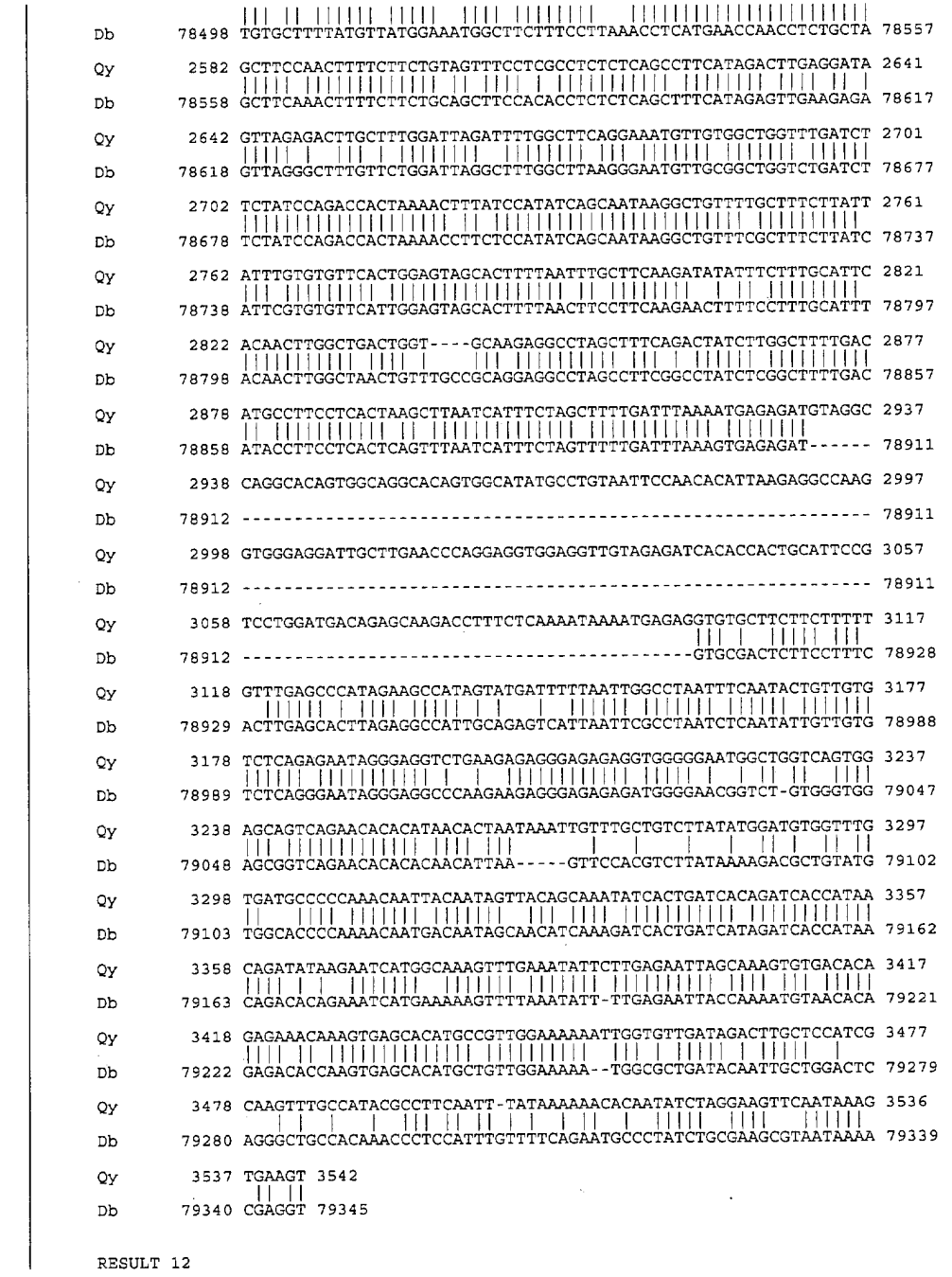
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Qy       1276 -CGGGGGTCAGGTGCTGAAGCTTAGGGTGGCTGTGGCAGTTTCTTAAA-----ACAACAG 1329
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Qy       1390 GCTTTTTGATAGCATTTTATGCACAGTAGAACTTCTTTGAAAATTGGA-TCAATCCTCTC 1448
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Db      77372 GCTGTTTGATAGCATTTTGCCCACAGTAGAGCTTCTTTCAAAATTGGAGTCAATCCTCTC 77431
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RESULT 12

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DEFINITION  Homo sapiens clone RP11-91N19, WORKING DRAFT SEQUENCE, 15 unordered
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ACCESSION   AC012033
VERSION     AC012033.20  GI:9966196
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 158276)
  AUTHORS   Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K.,
            Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
            Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
            David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,
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            Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A.,
            Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D. and
            Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 158276)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Sep 4, 2000 this sequence version replaced gi:9929521.
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                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: HMOR
                Center clone name: RP11-91N19
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 135987 bases at least Q40
                Consensus quality: 145984 bases at least Q30
                Consensus quality: 149762 bases at least Q20
                Estimated insert size: 149948; sum-of-contigs estimation
                Estimated insert size: 249006; agarose-fp estimation
                Quality coverage: 2.8x in Q20 bases; agarose-fp estimation
                Quality coverage: 4.6x in Q20 bases; sum-of-contigs estimation
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            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 15 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *   120424   130440: contig of 10017 bp in length
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            *   130541   135818: contig of 5278 bp in length
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            *   149761   150931: contig of 1171 bp in length
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            *   151032   152757: contig of 1726 bp in length
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  Best Local Similarity   74.8%;  Pred. No. 4.2e-205;
  Matches 1889;  Conservative    0;  Mismatches  411;  Indels  226;  Gaps   21;

Qy       1051 ATCACAATAAAGTGAGTCACA-CAAGTCTTTTGGCTTCCCAGTGCATATAAAAGTTTTGC 1109
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Qy       1167 ACCTTAATTTTAAAATGCTTTATTACTAAAAAATGCTAACAATC-ATTTGAGCATTCAGT 1225
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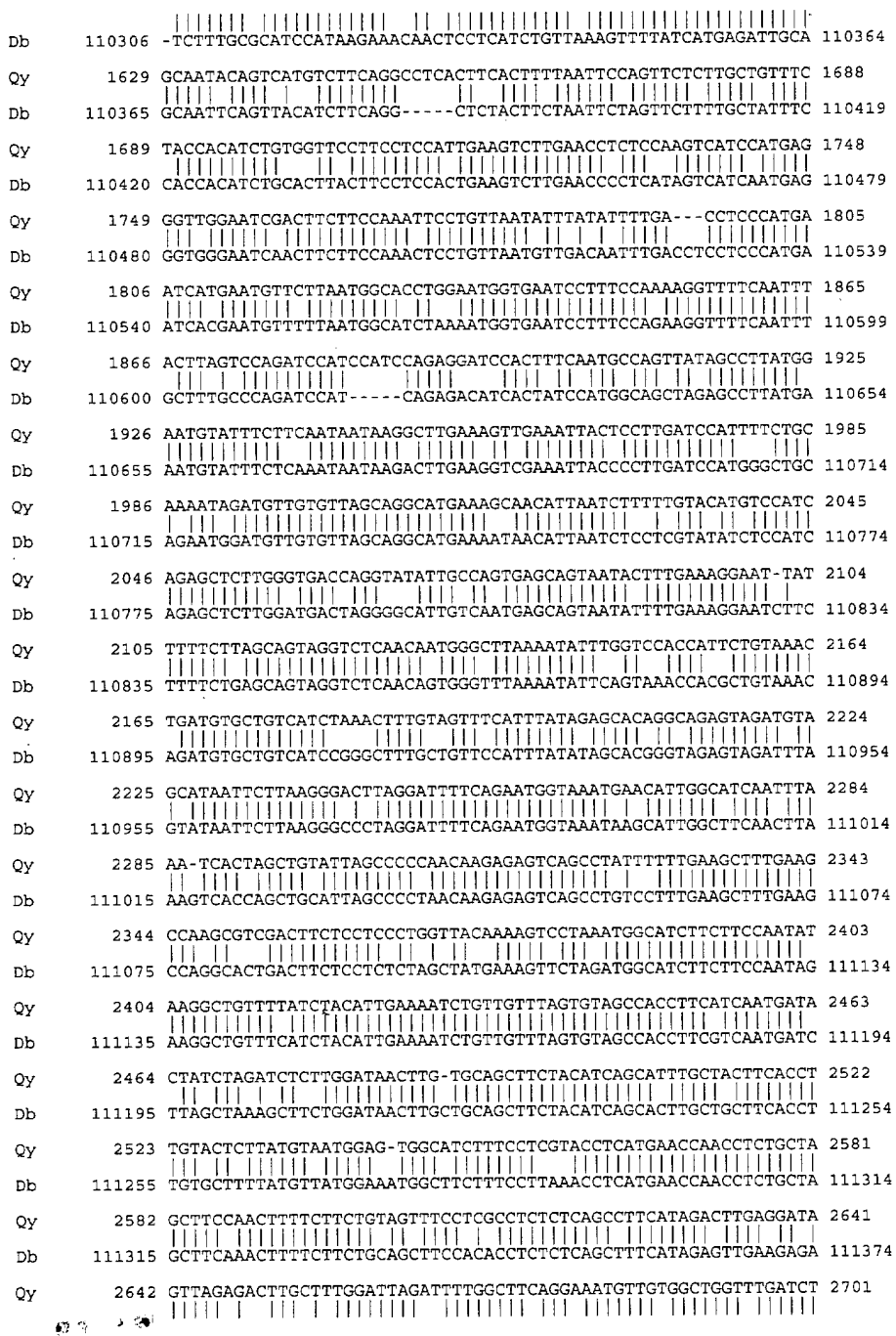
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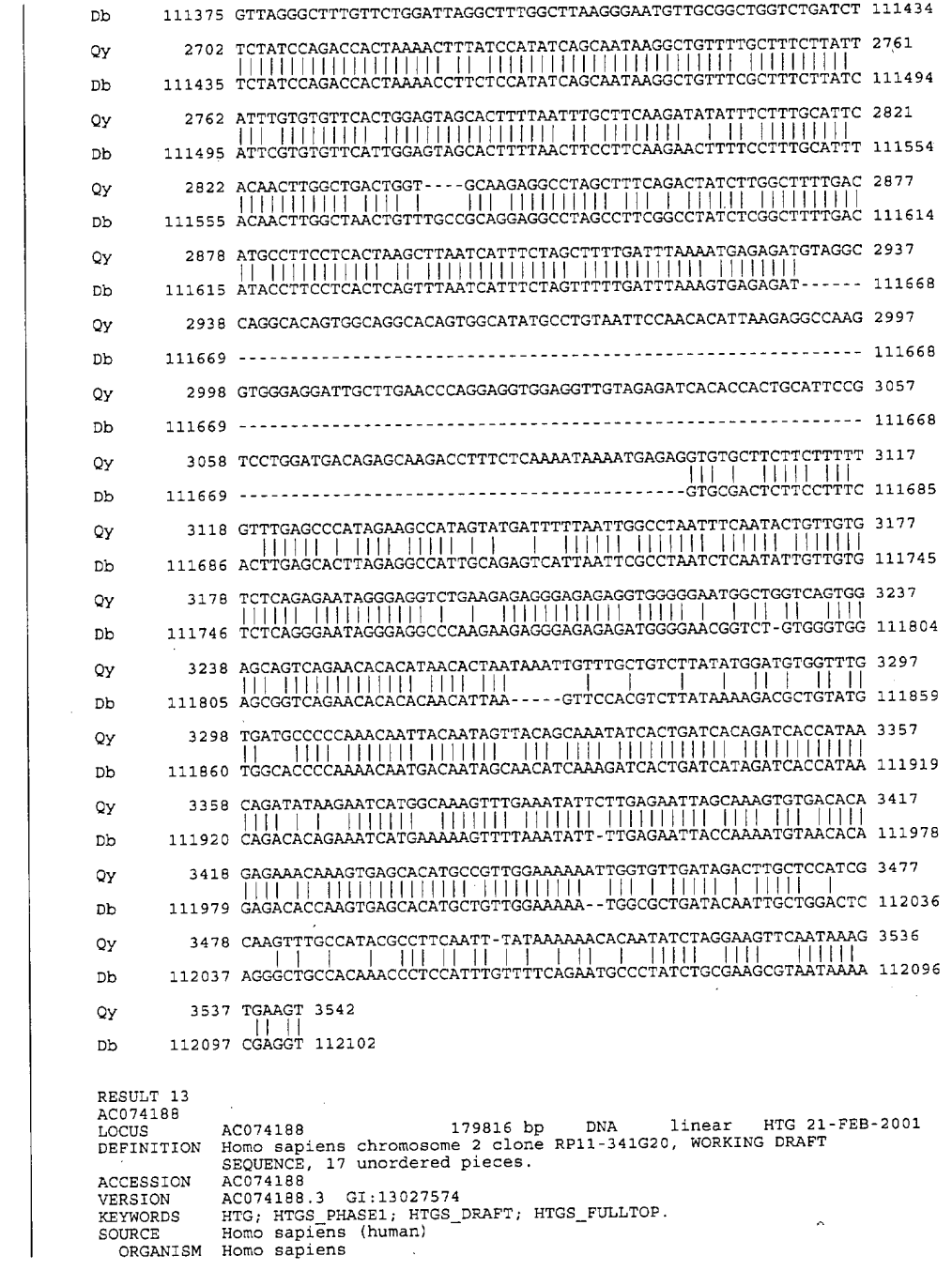
Qy       1390 GCTTTTTGATAGCATTTTATGCACAGTAGAACTTCTTTGAAAATTGGA-TCAATCCTCTC 1448
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Qy       1449 AAACCCTGCTCTGCTTTAACAACCTAAGTTAATATAATATTCTGAATCCATTGTTGTCAT 1508
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Db     110189 AAACCCTGCTGCTGCTTTATCAACTAAGTTTATGTAATATTCTAAATCCTTTGTTGTCAT 110248

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Qy       1569 ATCTTTGCTCATCCATAAGAAGAAATTCCTCATCTGTTCAAGTTTTATCATGAGATTGCA 1628
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RESULT 13
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LOCUS AC074188 179816 bp DNA linear HTG 21-FEB-2001
DEFINITION Homo sapiens chromosome 2 clone RP11-341G20, WORKING DRAFT SEQUENCE, 17 unordered pieces.
ACCESSION AC074188
VERSION AC074188.3 GI:13027574
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1  (bases 1 to 179816)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 179816)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Feb 21, 2001 this sequence version replaced gi:9802849.

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            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
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            Center project name: H_NH0341G20
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            Sequencing vector: M13; 94%
            Sequencing vector: plasmid; 6%
            Chemistry: Dye-primer ET; 94% of reads
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            Assembly program: Phrap; version 0.990319
            Consensus quality: 167169 bases at least Q40
            Consensus quality: 170689 bases at least Q30
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 17 contigs. The true order of the pieces
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            *    28568    36770: contig of 8203 bp in length
            *    36771    36870: gap of unknown length
            *    36871    48944: contig of 12074 bp in length
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            *   101708   120221: contig of 18514 bp in length
            *   120222   120321: gap of unknown length
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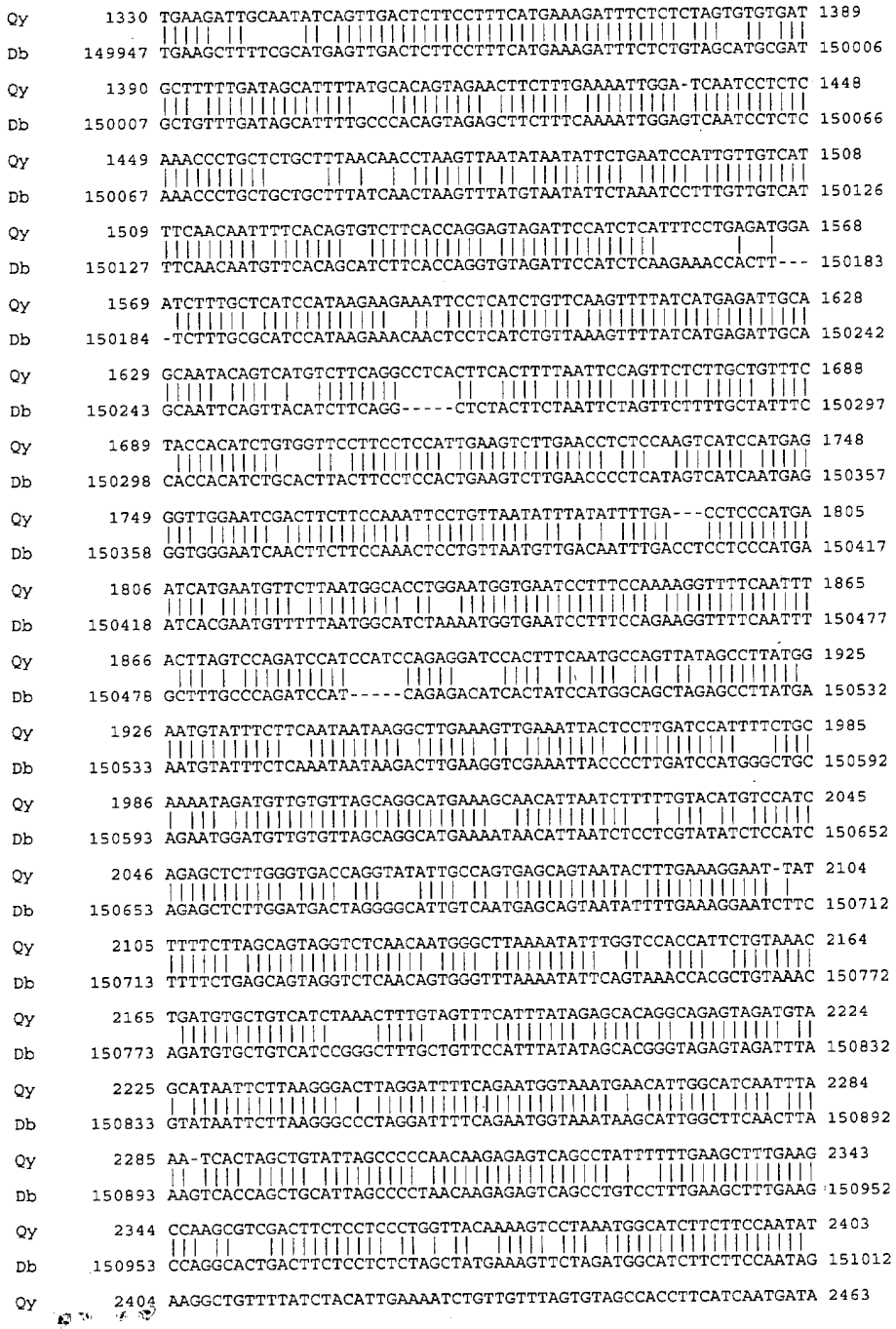
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RESULT 14
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LOCUS       BC035143               2641 bp    mRNA    linear   PRI 17-DEC-2003
DEFINITION  Homo sapiens cDNA clone MGC:43254 IMAGE:5264460, complete cds.
ACCESSION   BC035143
VERSION     BC035143.1  GI:23243251
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 2641)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2641)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 73 Row: j Column: 13
            This clone was selected for full length sequencing because it
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                     125 residues, there is a DNA-binding region, which binds
                     to a corresponding 17bp CENP-B box sequence. CENP-B dimers
                     either bind two separate DNA molecules or alternatively,
                     they may bind two CENP-B boxes on one DNA molecule, with
                     the intervening stretch of DNA forming a loop structure.
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     misc_feature    1206. .1931
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                     contain three carboxylate residues that are believed to be
                     responsible for coordinating metal ions needed for
                     catalysis. The catalytic activity of this enzyme involves
                     DNA cleavage at a specific site followed by a strand
                     transfer reaction. Interestingly this family also includes
                     the CENP-B protein. This domain in that protein appears to
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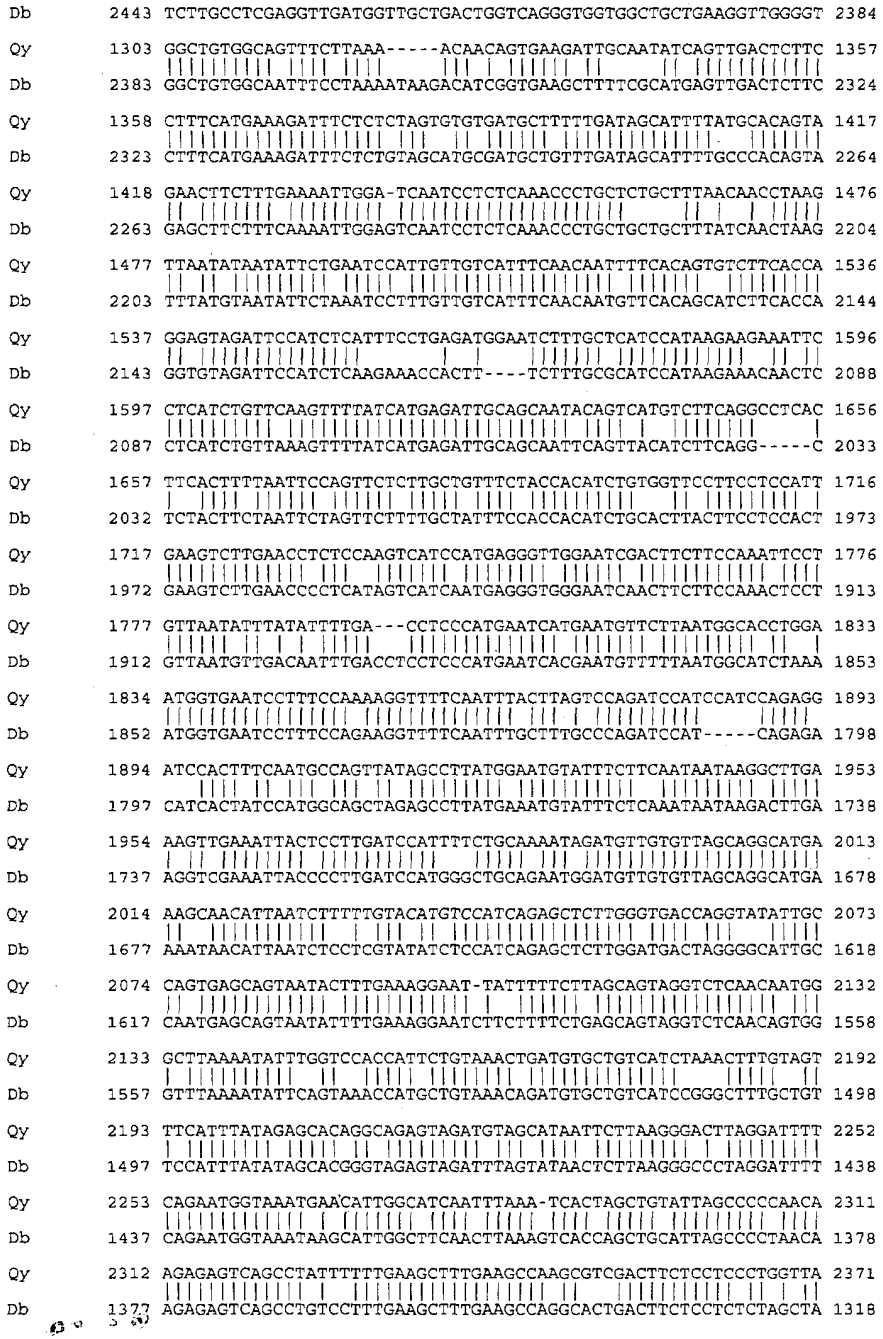
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RESULT 15
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LOCUS AC108017 51343 bp DNA linear PRI 27-MAR-2002
DEFINITION Homo sapiens BAC clone CTD-2005A22 from 4, complete sequence.
ACCESSION AC108017
VERSION AC108017.4 GI:19526131
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51343)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 51343)
AUTHORS Trani,L., Kozlowicz,A. and Dignan,G.
TITLE The sequence of Homo sapiens BAC clone CTD-2005A22
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 51343)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 51343)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 51343)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 51343)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Mar 16, 2002 this sequence version replaced gi:18873881.
---------- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
---------- Summary Statistics
Center project name: H_MS2005A22
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
Clone CTD-2005A22 is from a release of the human BAC library CTD. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
VECTOR: pBeloBAC11
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-719M18, 2000 bp overlap; the clone sequenced to the right is RP11-575B4, 2000 bp overlap. Actual start of this clone is at base position 120807 of RP11-719M18; actual end is at base position 7921 of RP11-575B4.

Polymorphisms have been identified between AC108017 and AC019341.

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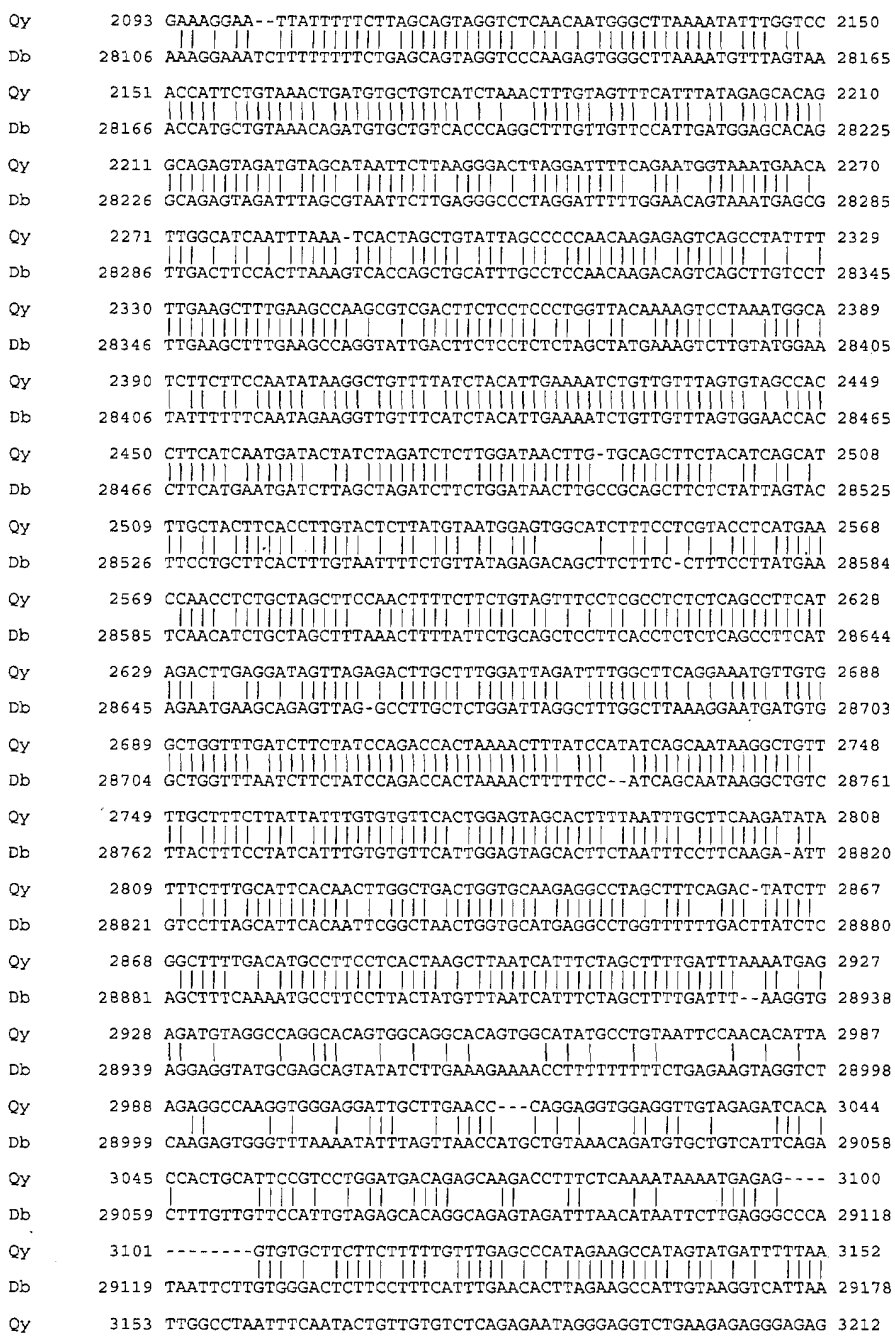
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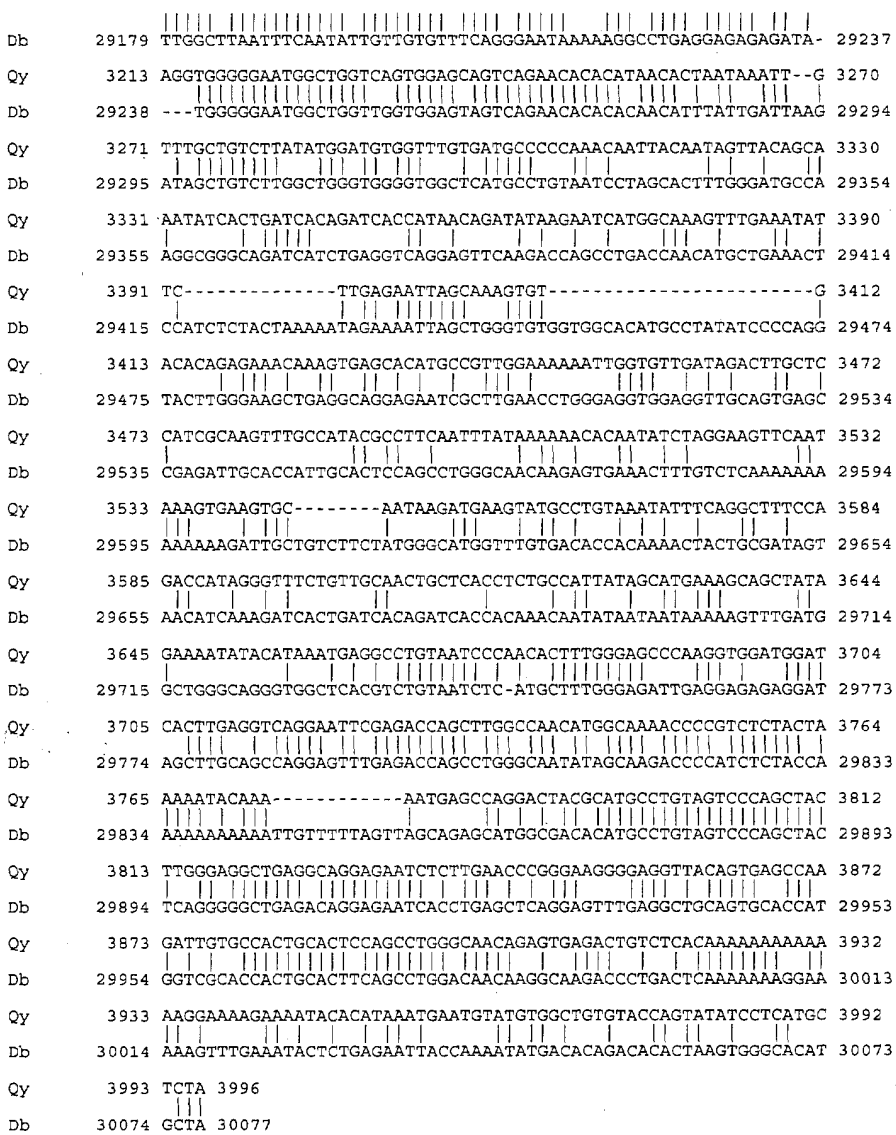
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